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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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1: gb_ba1:
2: gb_ba2:
US-09-477-392-1
2954
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_ba2:*
gb_om:*
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44: em_htg2:*
45: em_bum5:*
46: em_hum5:*
47: gb_p13:*
48: gb_pr5:*
49: gb_htg8:*
50: gb_htg10:*
51: gb_htg11:*
52: gb_htg11:*
55: gb_htg11:*
56: gb_htg11:*
57: gb_htg11:*
58: gb_htg11:*
69: gb_htg11:*
61: em_htg4:*
61: em_htg4:*
62: em_htg4:*
63: em_htg6:*
64: em_htg6:*
65: gb_htg10:*
66: gb_htg10:*
67: gb_htg10:*
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69: gb_htg21:*
70: gb_htg21:*
71: gb_v12:*
71: gb_v12:*
71: gb_v12:*
71: gb_p1:*
71: gb_
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	0.0	0	0.0	0	Ω ,	Re
18 19 20 21	13 14 15	11 12	1098	 7654	21	Result No.
279.4 278.4 278.4 278.4 278.4	304.6 299.8 283.6 282.8 281	315.2 310.4	315.8 315.8 315.4	2719.4 2654.6 1256.4 1194.8 719	2954 2729	Score
9.44.5	10.3 10.1 9.6 9.5	10.7 10.5	10.7 10.7 10.7	92.1 89.9 42.5 24.3	100.0	Query Match
295 2311 2416 2416		2382 130067	6045 185306 239566	2878 2878 179225 201458 759	2954 132150	Query Match Length
78 78 78 79	55 8 55 55 55		8 39 77	37 77 58 40 78	37	DB
HSG5 HSZNF74A3 HSZNF741 G27154	MMZFP29 AC012313 AC079575 AC004877 AC060772	AK023017 AC007228	AB002324 AC013570 HSAJ03147	AK025356 HSA245553 AC073111 AC015887 HSM802596	AF201303 AC005586	ID
X82192 H.sapiens E AF072567 Homo sapi X71623 H.sapiens Z G27154 SHGC-31580	X55126 M.musculus AC012313 Homo sapi AC079575 Mus muscu AC004877 Homo sapi AC060772 Mus muscu	AK023017 Homo sapi AC007228 Homo sapi	AB002324 Human mRN AC013570 Homo sapi AJ003147 Homo sapi	AKO25356 Homo sapi AJ245553 Homo sapi ACO73111 Homo sapi ACO15887 Mus muscu AL162065 Homo sapi	AF201303 Homo sapi AC005586 Homo sapi	Description

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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ACCESSION
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Primates
1 (bases 1 to 2954)
Houchens, C.R., Montigny, W.,
                                                                                                                                                                                                                                                                                                                                                  Submitted (02-NOV-1999) Pathology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heintz, N.H.
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chens,C.R., Gilbert,J.M. and
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RAHLRRCHPPAPEACHLCGSSFRGWALVLHHLAHSAAKQPIACPKCERRFRRKGL
RAHLRRCHPPAPEACHLCGSSFRGWALVLHIAHRRWHTGERPHOCPECGKRFRKK
RAHLRRCHPPAPEACHCGCRRFRHKPNLLAHKRWHTGERPHOCPECGKRFNK
PYLTSHRRIHTGEKPYPCKECGRRFRHKPNLLSHSKHIKRSEGSAQAAPGPGSPQLPA
GPQESAAEFTRAVELKPAQEPPPGAPEHPQDFLEAPPSLYSCDDCGRSFRLERFLAR
HQRHDTGERPFCAECGKNFGKKTHLVAHSPVHSGERPPACEECGRRFSQGSHLAAHR
RDHANDFBERPFTCAECGKNFGKKTHLVAHSPVHSGERPFACEECGRRFSQGSHLAAHR
RDHANDFBERPFTCAECGKNFGKKTHLVAHSPVHSGERPFACEECGRRFSQGSHLAAHR
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                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
130..1833
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AF161886 Homo sapi
AC016629 Homo sapi
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AC017629 Homo sapi
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AF05249 Homo sapi
AC071224 Homo sapi
AC013273 Homo sapi
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2040	GCCCTGCTAGCGAGAGAGGTCAACCCCGGTGGCCAGGGAACCCACTTCCAAGCGCAGGG	198:	Db
2040	gccctgctagcgagagaggtcaaccccggtggccagggaacccacttccaagcgcagg	198:	Qy
1980	. tggagtaggggacaatgggaatcctagaggggatggaagatgcgggggagtgagctgggtg 	1921	р _р 2у
NN	agagggctggggtccttcgtggtgggagtcgcagtgggctgggggtgcctgcc	8 8	p 94
1860	CTCCTGGCCCACCAGAAGAAGCACGATGTCTGAGACGGTGGGCGGGGCCGTGTTGGCTGA	œ	В
1860	tcctggcccaccagaagaagcacgatgtctgagacggtgggcgggggccgtgttggctg	180	Qy
1800 1800	. atccgggacggcgcttctgctgtgccatctgtggccagaccttcgacgacgaggagaga	174: 174:	д Q
42	CCCGACTGCGACCGCAGCTTCAGCCAGAAGTCCAACCTCATCACCCACC	.68	망
1680	CAGAAGTCCAACCTGGTGTCGCACCGGCGCATCCACACGGGGGGAGCGGCCCTACGCCTG	1621 1681	3 &
1680	, cagaagtocaacctggtgtcgcaccggcgcatccacacgggcgagcggccctacgcctgt		Qy
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6	GGGCCCGCCAGAGCACCCGCAGGACCCGATCGAAG	i N	Ĵ
1260	gggccccgccagagcacccgcaggacccgatcgaagcccccccc	1201	Qγ
1200	GAGTCCGCGGCCCAGCCCCGGCGGTACCTCTGAAACCGGCCCAGGAGCCGCCCCA	1141	DЬ
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1080	ggccgccgcttccggcacaaacccaacctgctgtctcacagcaagattcacaagcgatcc	102	B 8
1020	TATCTGACTTCGCACCGGCGATCCACACCGGCGAGAAGCCCTTACCCGTGCAAAGAGTT	9	В
1020	. tatctgacttcgcaccggcgcatccacaccggcgaga		Qy

041 ACGCCGGCCTCCAGCTGGTGTGTGTAAGGCTCCGTCCTGACTGCCCTGGAAAGGAAAAAAAA	041 ACGCCGGCCTCCACCTGGTGTGTGTAGGCTCCTGATGCCTTGTCCTTGCCTTGCCCTGGCTAGGTGTGTGCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCACTGCCCTTGCCCTTGCCTTGCCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCCTTGCTTAGGGCACCCCTTGCCTTGCTTAGGGCACCCCTTGCTTAAGTGCCCTTGCTTAGGGCACCCCTTGCTTAAGTGCCCTTGCTTAGGGCACCCCTTGCTTAAGTGCCCTTGCTTAAGTGCCTTTTAGGAAGCAAGGCATTACACCCTTGTTAAAGTGCCTTTAAATGCACCCTTGCTTAAATGCAATGCATTACACCACTTAACGCCTTGGTAAATGAATG	Qy Db	Оy	Оу	Qу	dg .	Qу Db	Qу	Qу	ОУ	Οy	ρb	Оу	Qу	Qу	Оу	da V
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RESULT 2
AC005586/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS
SOURCE

AC005586 132150 bp DNA PRI 30-SEP-2000 HOMO Sapiens PAC clone RP4-584D14 from 7q31-q35, complete sequence. AC005586 AC005586. 2 GI:8468933 HTG.

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REFERENCE
AUTHORS
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                                                                                                      This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                  University Genome Sequencing Center. For add
about the map position of this sequence, see
http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send
mailto:egreen@nhgri.nih.gov , or see http://s
                                                                                                                                                                                                                                                                                                                                             The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6.
On Jun 12, 2000 this sequence version replaced gi:3907529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 132150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
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Direct Submission
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Submitted (01-SEP-1998) Genome
University School of Medicine,
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Sulston, J.E. and Waterston, R.
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Mammalia; Eutheria; Primates;
                                                    The clone may be obtained either from Genome Systems, Inc
                                                                                   one male donor
                                                                                                                                                                                                                     SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAPPING INFORMATION:
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(http://www.genomesystems.com) or
(http://www.resgen.com); or from
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Contact: sapiens@watson.wustl.edu
------Summary Statistics
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                                                                                                                                                                                                                                                            or see http://genome.wustl.edu/gsc
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     Pieter
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NEIGHBORING SEQUENCE INFORMATION:

misc_feature

/note="similar to

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'note="match to EST AA129215 (NID:g1689084) zn84b02.s1"

EST AW246540 (NID:g6589533)"

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D
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                                                                                                                                                                                                                                                                                            /rpt_family="Alu" 6453. .6690
                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MIR" 5947. 5952
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1733. .2080
                                                                      /note="match to EST W72943 (NID:gl383235) zd54f12.r1" 7886 8357
                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_famil
5679. .577
/note="similar to
7886. .8403
                                                                                                           /note="match to EST AI144211 (NID:g3666020) qb93g11.x1"7883. .8397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                   /note="match to EST
7886. .8562
                                                                                                                                                                                                                       /rpt_family="Alu"
7008. .7117
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5148. .6450
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                                                        AI144211
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Matches 2796; Conserv
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/note="similar to 1
8743. .8744
                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to EST AI359215 (NID:g4110836) qy2
8835. 9229
/note="similar to Oryctolagus cuniculus EST C83534
(NID:g3062491)"
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/note="simil
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/note="match to EST AA059375 (NID:g1553199) zf66g07.rl"

8433. 8746
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/note="match to EST R72488 (NID:g846520) yj90g06.rl"
7976. .8575
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8707. .8845
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8591. _9167
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8228: .8562
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8192. .8564
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/note="similar to EST AA843440 (NID:g2929958) ak07h10.s1"
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99.1%;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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2 (bases 1 to 2878)
Sugano, S., Suzuki, Y.,
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                                     /organism="Homo sapiens"
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/clone="COLU9895"
/clone_lib="COL"
/tissue_type="colon"
/note="cloning vector pME
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1015 gagtgoggccgccgcttccggcacaaacccaacctgctgtctcacagcaagattcacaag 1074	790 CGCGTGCACAGGGGCGCCCCACCAGTGCCGATGCGGAAGGGCTTACCAAT 849 955 aagccctatctgacttcgaccggcgcatccacaccggcgagaagccctaccgtgcaaa 1014		75 cccaggggccgcccgcgggtgaccgcccccggcccggtggagatgccgtcgaccgccc 8	15 aagcgggtgcacgtagctgaggccctggaggaggccgcagccaaggctctgggggcccgg 7 	55 cccttcatatgcggcaactgtdgccggagctttgcccagtgggaccagctagttgcccac 71 	95 cgacgaaagcagcttcgagctcatctgcggcgttgccaccctcccgccccggaggcccgg 65 	535 ctggcccattcagctgcaaagcaacccatcgcttgtcccaaatgcgagagacgcttctgg 594	475 tttgcctgccacctctgtgggcagagcttccgaggctgggtggccctggttctgcatctg 534	415 catgcccccttcttagcactgcaccgccaggtccatgctgctgccacccccagacctgggc 474	355 accogcoggtgccaggcccggccttgcccttgcccttgcgctgtgtggccgtcgctttcgc 414	295 gcccatcgctgtgcccactgtcgaaggcacttccctggctgg	235 cgcgggctgaggcaacaaggcacgtcagtggcccagtctggtgcccaagccccaggcagg	175 cagccccgactcctttctgggccctcccaggagtcaccccagaccctggggaaggagtcc 234	115 gcagaggaagaaccgatgctggaacgtcgttgcaggggccccctggccatgggcctggcc 174	uery Match 92.1%; Score 2719.4; DB 37; Length 2878; est Local Similarity 98.6%; Pred. No. 0; entches 2806; Conservative 0; Mismatches 31; Indels 8; Gaps 6;	2 COUNT 560 a 974 c 826 g 518 t
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Homo sapiens |
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AJ245553.1 G
AP4 gene; AP4
                                     Eukaryota; Metazoa; Chordata; Craniata; Eukaryota; Metazoa; Chordata; Hominida; Eutheria; Primates; Catarrhini; Hominida; (bases 1 to 2878) Dobner, F.G., Fischer, M. and Groitl, P. Cloning of a novel zinc finger protein Unpublished
                     2 (bases 1 to 2878)
Dobner, T.G.
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NP4 protein;
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Consensus quality: 160317 bases at least Q40
Consensus quality: 166937 bases at least Q30
Consensus quality: 169751 bases at least Q20
Consensus quality: 169751 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 179255; sum-of-contigs
Quality coverage: 4.24 in Q20 bases; agarose-fp
Quality coverage: 4.40 in Q20 bases; sum-of-contigs
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3 (bases 1 to 179225)
4 (bases 1 to 179225)
5 (bases 1 to 179225)

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Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
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Center code: WUGSC
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Homo sapiens chromosome
31 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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7 clone RP11-511P7, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Mus musculus clone CT7-315E6, WORKING DRAFT SEQUENCE,
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                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M7815; 44% of reads sequencing vector: M13; M7815; 44% of reads sequencing vector: Plasmid; n/a; %-0.fx% of reads 55.55555555555556Chemistry: Dye-primer amersham; 58% (Chemistry: Dye-terminator Big Dye; 42% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 192611 bases at least Q40 Consensus quality: 196150 bases at least Q30 Consensus quality: 197810 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 19558; sum-of-contigs
                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                  be preserved.
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Contact: sequence_submissions@genome.wi.mit.edu
------Project Information
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1 1060: contig of 1060 bp in length
1061 1160: gap of 100 bp
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2601 2700: gap of 100 bp
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99251 129995: contig of 30745 bp
129996 130095: gap of 100 bp
130096 163192: contig of 33097 bp
163193 163292: gap of 100 bp
163293 201458: contig of 38166 bp
Location/Qualifiers
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13423 15194: contig of 1772 bp in length
15195 15294: gap of 100 bp
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is av
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This clone (DKFzp/62K135) is available at the RZPD in Berlin.
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/clone_lib="762 (synonym: hmel
DH10B; sites NotI + SalI"
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/tesue_type="melanoma (MeWo cu
a 246 c 252 g 144 t
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Eutheria;
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Pred. No. 1.2e-101;
0; Mismatches 10;
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(bases 1 to 6045)
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KIsarazu, Chiba 292, Japan (E-mail:cdnainfo@kazusa.or.jp,
ttp://www.kazusa.or.jp, Tel:+81-438-52-3930,
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                                         /POOLEL__G. BAA20784.1"
/POOLEL__G. BAA20784.1"
/POOLEL__G. BAA20784.1"
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IMGDPAQSPESKDSTEMSLERSSQDFSVPQNPPTPLGHSNPLDHQIPLDPCGKCFSFS
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SNLVQHQRTHTGEKPYKCTECEKAFTQSTNLIKHQRSHTGEKPYKCGECRRAFYRSSD
SNLVQHQRTHTGEKPYKCTECEKAFTQSTNLIKHQRSHTGEKPYKCGECRRAFYRSSD
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/clone="HG0579"
/clone_lib="pBluescriptII SK
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                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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IHTGEKPYKCSDCGKSFIRSSHLIQHRRTHTGEKPYKCPECGKSFSQSSNLITHVRTH
MDENLFVCSDCGKAFLEAHELEQHRVIHERGKYPARRAQGDSLLGLGDPSLLTPPPGA
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1514 þ a 1684 g 1072

10.7%;

Score 315.8; DB 8 Pred. No. 1.1e-39;

8

Length

6045;

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ggcgcatcggccggaccacgcccccgatcggcccttcgtgtgtcccgactgcggcaaggc
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                                                                                                                                                                                                                                                                                                 Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7654731. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                          Smit, A.F.A. & Green, F. (1220 1227)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates;
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Center project name: L2523
Center clone name: 2_C_24
Center clone name: 2_C_24
Center clone name: 1_C_24
Chemistry: Dye-terminator Big Dye; 10
                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                           Center code: WIBR
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                                                                                                                                                                              site: http://www-seq.wi.mit.edu
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RP11-2C24,
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DRAFT SEQUENCE,
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100% of reads
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CE, 37 unordered
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
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Insert size: 181706; sum-of-contigs
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6444: (
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1009 1108: gap of 100 bp
11109 2471: contig of 1363 i
2472 2571: gap of 100 bp
2572 4482: contig of 1071 i
4487 450
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100 bp

83219: contig of 5267 bp

20 83319: gap of 100 bp

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100 bp
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92 28391: gap of 1348 bp in 16
92 29839: gap of 100 bp
40 29839: gap of 100 bp
40 33467: contig of 3628 bp in 16
68 3567: gap of 100 bp
68 37139: contig of 3572 bp in 16
40 37239: gap of 100 bp
53 4152: gap of 3813 bp in 16
54 41052: contig of 3813 bp in 16
55 4504: contig of 4352 bp in 16
56 4504: gap of 100 bp
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13361: contig of 1084 bp

13461: gap of 100 hr

15267: con+:
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16785: contig of 1418 bp
16885: gap of 100 hm
18775: conti
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8858: gap of 100 bp
10776: contig of 1918 bp
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54949: contig of 4727 bp
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41153. .45504
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45605, .50022
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1196: gap of 100 bp
166295: contig of 15099 bp in
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                                                                                                                                                                             81025 CTCCACCTCATCAAGCACCAGCGGACTCACCTGCGCGAGGACCCCGTTCAAGTGCCCAGT
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 80845 CAACCACCAGCGCATCCACCGCGGCGAGCGCCCTACATCTGCGCCGACTGCGGCAAGAG
                                                                                                                                                                                                                                                                                                                      1171 cctctgaaaccggccaggagccgccgccaggggccccgccagagcaccc-gcaggaccc
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                  ggcgcatcggccggaccacgcccccgatcggcccttcgtgtgtccccgactgcggcaaggc
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                                                          CGAGCGGCCCTACAAGTGCCCAGAGTGCGGCAAGAGCTTCAGCGTCAGCTCCAACCTCAT 80846
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77953. .83219
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65176. .71663
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71764. .77852
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Pred. No. 4.8e-40;
0; Mismatches 517;
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Bernot.A., Heilig.R., Clepet.C., Smaoui.N., da Silva.C.,
Petit.J.L., Devaud.C., Chiannilkulchai.N., Fizames.C., Samson.D.,
Cruaud.C., Caloustian.C., Gyapay.G., Delpech.M. and Weissenbach.J.
A transcriptional Map of the FMF region
Genomics 50 (2), 147-160 (1998)
98317529
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Homo sapiens complete genomic sequence between D16S3070 and
D16S3275, containing Familial Mediterranean Fever gene disease.
AJ003147
                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-JAN-1998) GENOSCOPE - 2 rue Gaston Cremieux, EVRY BP191, ELocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HUMNK4 gene; mareno gene;
gene; olfactory receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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zinc finger protein; znfmf gene.
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VTIENDTPLEELSKYVDISIIALTRNRRTRRWYTCPLCGKQFNESSYLISHQRTHTGE KPYDCNHCGKSFNHKTNLNKHERIHTGEKPYSCSQCGKNFRQNSHRSRHEGIHIREKI FKCPECGKTFPKNEEFVLHLQSHEAERPYGCKKCGRRFGRLSNCTRHEKTHSACKTRK

-	1/92	/33 agagecaeateegggaeggeettetgetgtgeeatetgtggeeagaeettegaegaeg	OY 1/
	3		<u>.</u>
-	85		486
-	1732	73 acqcctqtcccqactqcqaccqcaqcttcaqccaqaaqtccaacctcatcacccacc	Qу 16
	1672 48659	513 cettcagecagaagtecaaectggtgtegeaecgggegeatecaeaegggegageggeeet	Qy 16 рь 487
	1612 48719	353 cgcggcaccggcgatccacaccggcgagaagccctacgtctgccccgactgcggcaaag 	Qy 15 Db 487
	7	38 GCCCTCGGCCCACTGCACCCAGTGCGGGAAGAGTTTCGGCCAGACCCAGGATCTG	8
	1552	93 cogatoggocottogtgtgtcccgactgcggcaaggccttccgccacaaaccctacc	Qy 14
	1492 48839	133 agtgcggccgccgcttctcccagggcagccatctggcggcgcatcggccggaccacgccc	Qy 14 Db 488
	1432 48899	373 agacgcacctggtggcgcactcgccggtgcactccggcggcgagcgccttcgcctgcgagg	Qy 13 Db 489
	48959	18 GGTGCACACGGGCGAGGCCTTCTCCTGCCAGGCTTGCGGCCGCAGCTTCACGCAG	Db 490
	1372	13 ggcacgacaccggggagcggccttcacctgcgccgagtgcgggaagaacttcggca	Оу 13
	1312 49019	53 acagotgogacgactgoggcaggagottco 	Qy 12 Db 490
	1252 49079	194 gccyccaggygccccyccagagcacccycaggacccy-atcyaagcccccccctcttt	·Qy 11 Db 491
	1193 49139	134 cccccaggagtccgcgagcccaccccggcggtacctctgaaaccggcccaggagcc 	Qy 11 Db 491
	1133 49199	074 gegateegagggteggeeeaggeegeeeggeeegggageeeeagetgeeageegg	Qy 10 Db 492
	1073 49259)34 ggcacaaacccaacctgctgtctcacagcaagattcacaa	Qy 10 Db 493
	1033 49319	974 accggcgcatccacaccggcgagaagccctacccgtgcaaagagtgcgcgccgcctcc	Qy 9 Db 493
	973 49379	914 ggccccaccagtgccccgagtgcgggaagcgctttaccaataagccctatctgacttcgc	Qy 9 Db 494
	913 49439	354 gcaagcgetteeggeacaageecaaettgategeteacegeeggegtgeacaegggegage	Qy 8 Db 494
	853 49499	794 tgaccgcccccggccggtggagatgccgtcgaccgcccttccagtgtgcctgttgtg	Qy 7 Db 495
ω ``	ps	y Match 10.7%; Score 315.4; DB 77; Length 239566; Local Similarity 58.5%; Pred. No. 5.2e-40; hes 616; Conservative 0; Mismatches 416; Indels 21; Ga	Query Best Match

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REFERENCE
AUTHORS
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  CGCGTTCATCTTACACCAGAGAATCCACACCGGGGAGAAGCCATTTGCGTGCCCCGAGTG
                  caacttgatcgctcaccgcgcgtgcacacgggcgagcgcccaccagtgccccgagtg 935
                                                        TGGAGGCCCCAAGAAGCCGTGGAAATGCGGGGACTGCGGGAAGGCCTTCAGCTACTGTTC
                                                                                                              ACGCGCATCTGCGGCGCGCACCTGGCTACCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                              NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. To Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951), Fax:81-438-52-3952)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki
Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K.,
Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Ishii,S., Kawai
Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens cDNA FLJ12955 fis,
similar to ZINC FINGER PROTEIN
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Isogai, T. and Otsuki, T.
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/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."
1 789 c 656 g 450 t
                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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caacctcatcacccaccgcaagagccacatccgggacggccttctgctgtgccatctg 1772
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Metazoa; Chordata; Craniata;

Vertebrata; Euteleostomi;

130067 bp s chromosome

DNA 19, BAC

37295 (CIT-B-21A4), complete

06-APR-1999

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JOURNAL REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                              /rpt_family="Aluy"
complement(4953...4996)
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complement(5673...5793)
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                                 /rpt_family="MER58B"
complement(9302..9497)
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/rpt_family="L1MB5"
5864. .5996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFKCKECGKAFRONIHLASHLRIHTGEKPFECAECGKSFSISSQLATHQRIHTGEKPY
ECKVCSKAFTOKAHLAGHQKTHTGEKPYECTECKECGKAFSOTTHLIHGHQRVHTGEKPYKCY
MECGKAFGDNSSCTOHORLHTGORPYECT ECGKAFKTKSSLICHRRSHTGEKPYECSY
CGKAFSHRQSLSVHQRIHSGKKPYECKECRKTFIQIGHLNQHKRVHTGERSYNYKKSR
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join(332. .509,682.
6894. .8266)
                                                                                                            /rpt_family="MIR"
complement(8977.
                                                                                                                                                                                                                   /rpt_family="L1MA9"
complement(6099. .64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD23606.1"
/protein_id="AAD23606.1"
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/Clone_lib="CIT-B Cal Tech BAC library"
/note="LLNL Clone Name: BC37295"
complement(4___320)
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/db_xref="taxon:9606"
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/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 57.000"

complement(20721...20768)

/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000"

complement(21509...21720)

/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MLT1A2"
19599...19622
/rpt_fam
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/rpt_family="AluSg1"
complement(10096. .10278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(21729. .21817)
/rpt_family="MIR"
21897. .21996
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/note="BLASTN similarity to G44255 (13...186); match: 0.99, score: 1.3e-63; database searched: month.na; WIAF-3903-STS Human Thudson SANGER Homo sapiens STS genomic, sequence tagged site [Homo sapiens]"

complement(17491...17766)

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                                                                                                                                                                                                                                          EKPYECIECGKAFSDCSSLAHHRRIHTGKRPYECIDCGKAFRQNASLIRHRRYYHTGE
KPFDCIDCGKAFTDHIGLIQHKRTHTGERPYKCNVCGKAFSHGSSLTVHQRIHTGEKP
YECNICEKAFSHRGSLTLHQRVHTGEKPYECKECGKAFRQSTHLAHHQRIHTGEKPYE
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complement/??...18156)
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/rpt_family="(GGAA)n"
/rpt_family="AT_rich"
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                                                                                                                                                                                                                                                                                                                     /translation="MKSQEEVEVAGIKLCKAMSLGSVTFTDVAIDFSQDEWEWLNLAQ
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22540. .22611
/rpt_family="AluJo"
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/rpt_family="MLT1-INTERNAL"
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complement(1610)
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/rpt_family="AluJb"
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join(23186. .23245,27268. .27607,30057.
/note="Hypothetical ZNF-like human prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family-"MLT1-INTERNAL"
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lement/1227
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Query Match 10.5
Best Local Similarity 56.2
atches 603; Conservative
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                                                                                                                                                                                                                                                                                                                        agatgccgtcgaccgcccttccagtgtgcctgttgtggcaagcgcttccggcacaagcc
CCACTGGCGCACGCACGGGCGAGAAGCCGCACCGCTGCGCCGACTGCGGCAAGGCCTT
                                 tcacagcaagattcacaagcgatccgaggggtcggcccaggccgcccccggcccggggag
                                                                       GAAGCCCTACGCCTGCCACGAGTGCGGCAAGGCCTTCAGCCAGGGCCTCGTACCTGGCGTC
                                                                                                                                                 CGGCAAGGCCTTCAGCCAGAGCGTGCACCTGACCCTGCACCAGGCGCACACGCGCGA
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/complement(33334. 33460)
/rpt_family="LIMB6"
34364. 3446F
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complement(32802. .32984\
/rpt_family="x".
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35434. .35813
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/rpt_family="AT_rich"
complement(28510. .28645)
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/rpt_family="(GAAAA)n"
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/rpt_family="MIR"
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complement(32604. .:
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/rpt_family="(GAA)n"
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X55126.1
                         Denny, P. and Ashworth, A.
A zinc finger protein-encoding
phase of spermatogenesis
Gene 106 (2), 221-227 (1991)
                                                                                      Chester Beatty Laboratories, 2 (bases 1 to 2094)
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Rođentia; Sciurognathi; Muridae; Murinae;
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M.musculus Zfp-29
                                                                                                                    Submitted (03-NOV-1990) Denny
                                                                                                                                    Direct Submission
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                  cctgcgggcccaccagcggcacgacaccggggagcgccttcacctgcgccgagtgcgg 1355
                                                                                              agccccccccctctacagctgcgacgactgcggcaggagcttccggctggagcgctt 1295
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/note="zinc fingers"
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TECGQKFSQSSALITHRRTHTGEKPYCGECGKNESSSNLATHRRTHLYEKPYKCGL
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FSWNSVLIHQRIHTGEKPYRCPECGKGFSNSSNFITHQRTHLKEKLY"
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OEDGPESEPFPQSaGKGSPQEEDAAEGPQGALVRFRELCRRWLRPEVHTKEQMLTVLP
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LNISGGEGGQOSDGDSDFERDCSGGAAGHAPGEDPRVVPSEGREVGQLIGLQGTYLG
EKPPECPQCGKTFSKKSHLITHERTHTGEKYRCDECGKSFSDGSNFSHAHQTTHTGEK
EKPPECPQCGKTFSKKSHLITHGTHTGEKPFQCAECGKSFSRSPNLIAHQRTHTGEKPY
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104. .1948
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/db_xref="taxon:10090"
/dev_stage="adult male"
/tissue_type="testis"
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Consensus quality: 175352 bases at least Q40

Consensus quality: 181475 bases at least Q20

Consensus quality: 182252 bases at least Q20

Estimated insert size: 194270; agarose-fp estimation

Estimated insert size: 194270; agarose-fp estimation

Quality coverage: 8.32 in Q20 bases; agarose-fp estimation

Quality coverage: 8.82 in Q20 bases; sum-of-contigs estimation

Quality coverage: 8.82 in Q20 bases; num-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* in Faliance to be contigned as the content of the pieces
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AC012313.5 GI:7711546
DRAFT.
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Center Project Name: 835906, BC800930
Center clone name: CITB-E1_2619J13
                                                                                                                                                                                                                                                                                                                                                Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.ga
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-OCT-1999) Production Sequencing Facility, DOE Jo Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On May 6, 2000 this sequence version replaced gi:7690197.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 183525)
DOE Joint Genome Institute.
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believed to be correct as given, however the sizes
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                                                                                                                                                                                                                                                                                                                                                http://www.jgi.doe.gov
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Catarrhini; Hominidae;
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CTD-2619J13,
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BASE COUNT
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                   agctgccag-----ccggccccccaggagtccgcggccgagcccaccccggcggtacctct
                                                                                                                                                                                                                                                                                                                                         gcaagattcacaagcgatccgaggggtcggcccaggccgccccggcccggggagcccc
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GCTGCGGCAGCACCGGCACGCACAGCAGCGAGAAGCCCCTTCCCCTGCGCCGAGTGCGG
                                                                         GGGACTGTGGCAAGGCCTTCAGCCAGAGCTCCAACCTGGCCGAGCACCTGAA--GATCCA
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* This sequence will be replaced

* by the finished sequence as soon as it is available the accession number will be preserved.

1 23743: contig of 23743 bp in length

23744 23843: gap of unknown length

23844 34638: contig of 10795 bp in length

34639 34738: gap of unknown length

34639 34738: gap of unknown length
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48585 c 48353 g 43444
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/clone="CTD-2619J13"
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/db_xref="taxon:9606"
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8: contig of 32267 bp in length
8: gap of unknown length
6: contig of 5538 bp in length
6: gap of unknown length
1: contig of 725 bp in length
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* NOTE: This is a 'working draft' sequence. It currently estimation.
                                                                                                                                                                                            Center Project Name: 1769997
Center clone name: RPCI-23_86E5
                                                                                                                                                                                                                                                                                                                                    Submitted (02-SEP-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Search completed: February 22, 2001, 03:04:53 Job time: 14351 sec

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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                      NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Translation of Medical Science,
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HSA245553 Homo sapiens mRNA for I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Mikrobiologie und Hygiene, Universitaet Regensburg, Franz-Josef-Strauss-Allee 11, 93053 Regensburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2878)
Dobner, T.G., Fischer, M.
Cloning of a novel zinc
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AJ245553
                                                                                                                                                                                                                                                                                                                           Dobner, T.G.
Direct Submission
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AP4 gene; A
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                                                                                                                                            106.
                                                                                                  /gene="AP4"
106. .1776
                                                                                                                                                                                                                                             Location/Qualifiers
                                       /codon_start=1
                                                          /note="zinc finger protein"
                                                                             /gene="AP4"
                                                                                                                                                             /cell_line="HeLa"
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/db_xref="taxon:9606"
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REFERENCE AUTHORS

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AF201303
AF201303.1 G
                                                                                   Heintz,N.H.
The dhfr oribeta-binding protein RIP60 contains 15 zinc fingers:
DNA binding and looping by the central three fingers and an
associated proline-rich region
Nucleic Acids Res. 28 (2), 570-581 (2000)
Direct Submission
Submitted (02-NOV-1999) Pathology, University of Vermont,
Medical Alumni Building, Burlington, VT 05405, USA
Location/Qualifiers
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2954)
                                                                                                                                                                                                           Homo sapiens
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                                                     Houchens, C.R.,
                                                                                                                                                        Houchens, C.R., Montigny, W.,
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                                                 (bases 1 to 2954) chens, C.R., Gilbert, J.M. and
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CDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV"
1973 c 839 g 538 t
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Eukaryota; Metazoa; Chordata; Cri
Mammalla; Eutherla; Primates; Cai
1 (bases 1 to 132150)
Sulston, J.E. and Waterston, R.
Toward a complete human genome se
Genome Res. 8 (11), 1097-1108 (1)
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VAQSGAQAPGRAHRCAHCRRHPPGWVALWLHTBRCQARLPLPCPECGRRFRHAPFLAL
HRQVHAAATPDLGFACHLCGQSFRGWVALWLHTBRCARHCPLPCPECGRRFRHAPFLAL
HRQVHAAATPDLGFACHLCGQSFRGWVALWLHLLAHSAAKQP LACPKCERRFWRKQL
RAHLRRCHPPAPEARPTICGNCGRSFRAQWDQLVAHKRVHVAEALEEAAKAKLGPPRRG
RPAVTAPRPGGDAVDRPFQCACGKRFRHKPNLLAHRRVHTGERPHQCPECGKRFTNK
RYLTSHRRIHTGEKPYPCKECGRRFHKKPNLLSHSKIHKRSEGSAQAAPGPGSPQLPA
GPQESAAERTPTAVPLKPAQEAPPEHPQDPIEAPPSLYSCDAQAAPGPGSPCLRRFLRA
GPQESAAERTTQAVPLKPAQEAPPHPQDPIEAPPSLYSCDAGRSFRLERFLRA
HQRHDTGERPTTCAECGKNTGKKTHLVAHSPVHSGERPFACEBCGRRFSQGSHLAAHR
PDHAPDRFFVCPDCGKAFRHKPYLARHRRIHTGEKPYVCPDCGKAFSQKSNLVSHRRI
HTGERPYACPDCDKSFSQKSNLITHRKSHIRGERFTACTGTFDDEERLLAHQKKHD
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/protein_id="AAF26712.1"
/db_xref="GI:6716714"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1e-57;
); Mismatches 0;
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RP4-584D14 from
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                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                              MO 63108, 5 (bases
                                                                        Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jun 12, 2000 this sequence version replaced g1:3907529.
                                                                                                                                                                                                                              Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                        Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 132150) Waterston, R.H.
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Stoneking,T., Ozersky,P., Wohldmann,P. and Le,T.
The sequence of Homo sapiens PAC clone RP4-584D14
                                                                                                                                                                                                                                                                                            Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                  Submitted (01-SEP-1998) Genome University School of Medicine,
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                      Center: Washington University Genome Sequencing Center Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions

Center project name: H_DJ0584D14

Summary Statistics

USA

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this Clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc and

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from is from

one male donor.

The clone may be obtained either from Genome Systems, (http://www.genomesystems.com) or Research Genetics, I Inc.

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D14.

The sequence RP4-584D14 from base position 21655 to 22775 is rich. This region was sized with PCR from genomic DNA and the hindili digest with band size 3643 real, and 3642 insilico. the GT

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                                                                                                                                     /note="similar to 7886. .8451
                                                                                                                                                                           7886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4882.
                                                                                                                                                                                                                                             /note="match
7886. .8357
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                                                                                                                                                                                                                                                                                /note="match to EST AI144211 (NID:g3666020) gb93g11.x1" 7883. .8397
                                                    note="similar to"
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/clone_lib="RPCI-4"
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                                                                                                                      'note="match to
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/db_xref="taxon:9606"
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                EST H37790 (NID:g907289) yp46h05.s1"
                                                                                                                      EST AA129215 (NID:g1689084) zn84b02.s1"
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                                                  EST A1868891 (NID:g5542895) wc49f12.x1"
                                                                                                                                                                                         EST AW411281 (NID:g6936822) fh11d05.y1
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                                                                                                                                                                                                                           (NID:g3666020) qb93g11.x1"
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                                                                          gggagcccccagctgccagccggcccccaggagtccgcggccgagcccaccccggcggta
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                                                                                                                                                                                                                                           GAGTGCGGGAAGCGCTTTACCAATAAGCCCTATCTGACTTCGCACCGGCGCATCCACACC
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                                                            GGGAGCCCCCAGCTGCCAGCCGCCCCAGGAGTCCGCGGCCGAGCCCACCCCCGGCGGTA
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8228. .8362
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/note="similar to Oryctolagus cuniculus
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8754. .9069
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8616. .9159
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8463. .8928
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/note="similar
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Pred. No. 2.4e-58;
Mismatches 0;
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NOTE: This is a 'working draft' sequence. It currently NOTE: This is a 'working draft' sequence of the pieces consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 201458)
Birren, B., Linton, L.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Center clone name: 315_E_6
Center clone name: 315_E_6
Center clone name: 315_E_6
Center clone name: 315_E_6
Center clone name: M15_E_6
Center clone name: Statistics
Sequencing vector: M13_M77815; 44% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
55.5555555555556Chemistry: Dye-primer-amersham; 58
Chemistry: Dye-terminator Big Dye; 42% of reads
Assembly program: Phrap; version 0.960731 Consensus quality: 192611 bases at least Q40 Consensus quality: 196150 bases at least Q30 Consensus quality: 197810 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 199558; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.
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30950. .44871
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61355. .74139
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Location/Qualifiers
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13322: contig of 2703 bp in
13422: gap of 100 bp
15194: contig of 1772 bp in
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30849: contig of 6712 b
30949: gap of 100 bp
44871: contig of 13922
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74139: contig of 12785 bp in
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24037: contig of 3644 bp in length
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18405: contig of 3111 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens mRNA; cDNA ALI62065
                                                 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available.
                                                                                                                                                              Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                 at http://www.mips.biochem.mpg.de/proj/cDNA/
                                                                                                           This clone (DKFZp762K135) is available at the RZPD in Berlin
                                                                                                                               Braunschweig/Germany) within the German Genome Project.
                                                                                                                                                                                                                                Submitted (15-MAR-2000) MIPS, Am Klopferspitz 18a, Martinsried, GERMANY
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 759)
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74240. .99150
/note="assembly_fragment"
99251. .129995
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130096. .163192
                 Location/Qualifiers
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Pred. No. 1.1e-34;
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                                                                                                                                                   cDNA sequencing consortium
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/organism="Homo sapiens" /db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199;
                                                                         Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Sep 19, 1948 the sequence version replaced gi:3213120.
                                                                                                                                                                    Submitted (19-SEP-1998) Department of University, 4444 Forest Park Avenue, 4 (bases 1 to 128361)
                                                                                                                                                                                                                                                                                        Submitted (12-JUN-1998) Genome University School of Medicine,
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Homo sapiens PAC clone
                                                                                                                                                       Waterston, R.
                                                                                                                                                                                                                          Direct Submission
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The sequence of Homo sapiens PAC clone RP4-751H13
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                                                                                                                                                                                                                                                                                                                                              Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Leonard, S., Graves, T.
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                 Center: Washington University Genome Center code: WUGSC
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/clone_lib="762 (synonym: hmel2).
DH10B; sites NotI + SalI"
/dev_stagė="adult"
/tissue_type="melanoma (MeWo cell
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                                                                   -- Genome Center
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67.9%;
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Pred. No. 4.3e-16;
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                                                                                                                                                                                    Genetics, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7q35-qter,
                                                Sequencing Center
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Missouri 63108,
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                                                                                                                                                                                                                                                                                          Louis
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Center project name: H_DJ0751H13

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Bric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information MAPPING INFORMATION: mapping and Mapping

The clone sequenced to the left is RP4-811N16, Actual start of this clone is at base position actual end is at 128361 of RP4-751H13.

Location/Qualifiers
1. .128361

FEATURES

misc_feature misc_feature misc_feature repeat_region misc_feature repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region source repeat_region repeat_region /rpt_family="L2" 9100. .9426 /note="match to EST 10297. .10734 /note="match to EST 9947. .10370 /clone_lib="unknown"
20. .155 /rpt_family="L1" 12222. .12615 /rpt_family="MaLR" 11605. .12220 /note="match to EST AA828832 (NID:g2901931) od80c03.sl" complement(9947. /map="7q35-qter" /clone="RP4-751H13" /db_xref="taxon:9606" /chromosome="7" /rpt_family="Alu" /note="match to EST 'rpt_family="Retroviral" 'rpt_family="Alu" organism="Homo sapiens" 'note="match to EST rpt_family="MIR" rpt_family="MaLR" rpt_family="L2" 'rpt_family="MER1_type?" rpt_family="Alu" _family="Retroviral" _family="Alu" .8311 . 7870 . 2885 . 4287 .10086 .10370) AA828832 (NID:g2901931) od80c03.s1 AA080867 (NID:g1623560) AA084720 (NID:g1626811) zn06f02.s1" AA857387 (NID:g2945689) od83h10.s1

zn06f02.rl"

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complement(20009. 21523)
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H_DJ0755H13.3"
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                                                                                                                                                                                                                                                                                                                                                                                            /translation="MIRKVKVEDEDQEAEEEVEWPQHLSLLPSPFPAPDLGHLAAAYK LPGARGALSGLALSGGMEPMPKFYGGGECERRFROOLT/IRLIGHRAHMEREPPGPCACPDC GRSTTORAHMLLHQRSHRGERPFPCSECDKRFSKAHLTHLRTHTGERPYPCAECGK RFSQKIHLGSHQKTHTGERPPPCTECEKRFRKKTHLIHQRIHTGERPYQCAQCARSF RFSQKIHLGSHQKTHTGERPPFCTECEKRFRKKTHLIHQRIHTGERPYGCAQCARSF TKKOHLVRHQRVHQTAGPARRSPDSSASPHSTAPSFTPSFFGFKFFACSDCGLSFGWKTHKOHLVRHQRVHQTAGPARRSPDSSASPHSTAPSFTPSFFGFKPFACSDCGLSFGWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CpG_1sland (%GC=70.4, o/e=0.70, #CpGs=171)" complement(19861. 20173) /note="match to EST AA923119 (NID:g3070428) ok91e12.s1" 19861. 20239
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20819. .21219
                                                                  20298. .20740
/note="similar to Mus musculus EST AA021873 (NID:g1485629)
                                                                                                                                                                                                                                                           /gene="WUGSC:H_DJ0751H13.3"
/note="match_to_EST_AA771702 (NID:g2823485) ai32a10.s1"
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/db_xref="GI:3638956"
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                                                                                                             note="match to EST AA894411 (NID:g3030812)
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12617. .12755
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AUTHORS
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20961 AGCGCTTTCGCAAGAAGACGCACTTGATTCGGCACCACGCCATTCCATACGGGCGAGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCTCGCACCAAAAGACCCACACCGGCGAGCGGCCCTTCCCCTGCACGGAATGCGAGA
Submitted (05-NOV-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jul 15, 2000 this sequence version replaced qi:8990985.
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210923)
Waterston,R.H.
                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                         2 (bases 1 to 210923)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                          AC013273.5 GI:9211421
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                              The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome
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24983
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23773
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26933. .29260
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24894. .24982
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23679
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7 clone RP11-428D5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA757828 (NID:g2805691) zg44d02.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORKING DRAFT SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Summary Statistics

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer ET; 74% of reads
Chemistry: Dye-terminator Big Dye; 26% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 200959 bases at least Q40
Consensus quality: 204292 bases at least Q30
Consensus quality: 206312 bases at least Q30
Consensus quality: 206312 bases at least Q20
Insert size: 203000; agarose-fp
Insert size: 210023; sum-of-contigs
Quality coverage: 4.85 in Q20 bases; agarose-fp
Quality coverage: 4.93 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; 74% Sequencing vector: plasmid; 26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       runs of \tilde{N}_{\rm r} but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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11908
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29299
29399
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63663
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                                                                                                                                                                                                                                                                                                                                                                /note="assembly_name:Contig9"
4718. .11807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                 vector_side:left"
                                                                                                                                                                                       /note="assembly_name:Contigl3"
45801. .63662
                                                                                                                                                                                                                                                             clone_end:T7
                                                                                                                                                                                                                                                                                                                               11908
                /note="assembly_name:Contig17" 51422 c 51731 g 52663 t
                                                    /note="assembly_name:Contig16"
150744. .210923
                                                                                                                                                      clone_end:SP6
                                                                                                                                                                                                                                      vector_side:right"
                                                                                    /note="assembly_name:Contig15"
104608. .150643
                                                                                                                                                                     /note="assembly_name:Contig14
                                                                                                                                                                                                                                                                        /note="assembly_name:Contigl2
                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contigl1"
                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-428D5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location
                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45700: contig
45800: gap of
63662: contig
63762: gap of
104507: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150743: gap of 
210923: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104607: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2429:
                                                                                                                      .104507
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gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 60180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 8557
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of 7090
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of 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 16302 bp in
unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 46036 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 8734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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TITLE
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DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
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                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTACCAGTGCGCACAGTGCGCACGCAGCTTCACGCACCAGCAGCACCACTTGGTGCGGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agcgctttaccaataagccctatctgacttcgcaccggcgcatccaccaccggcgagaagc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phase of spermatogenesis
Gene 106 (2), 221-227 (1991)
92039080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Denny, P. and Ashworth, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chester Beatty Laboratories, 2 (bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-NOV-1990) Denny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denny,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spermatogenesis; Zfp-29 gene; zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X55126.1 GI:55470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  finger protein-encoding gene
                                            /gene="Zfp-29"
/gene="Zfp-29"
/codon_start=1
/codon_start=1
/protein_id="Caa38920.1"
/protein_id="Caa38920.1"
/db_xref="GI:55471"
/db_xref="SWISS-PROT:007230"
/d
EKPYECPQCGKTFSRKSHLITHERTHTGEKYYKCDECGKSFSDGSNFSRHQTTHTGEK
PYKCRDCGKSFSRSANLITHQRIHTGEKPFQCAECGKSFSRSPNLIAHQRTHTGEKPY
                                                                                                                                                                                                                                                                                                                   /gene="Zfp-29"
104. .1948
                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="testis"
/clone_lib="Lambda ZAP cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="ssp. domesticus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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); Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 126.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed
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Best Local Sim
Matches 195;
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                                                                                                                                                            Submitted (14-JUN-2000) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway, MO 63108, USA On Jul 7, 2000 this sequence version replaced gi:8516162.
                        Center project name: H_NH0143I21
                                                                                       Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, 6 unordered pieces. AC073314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing
                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                         Waterston, R.H.
                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                          The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                              Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT
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/note="zinc fingers"
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KGFSQRSQLVVHQRTHTGEKPYKCLMCGKSFSRGSILVMHQRAHLGDKPYRCPECGKG
vector: M13; 66%
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Pred. No. 2.4e-13;
0; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone RP11-143I21,
                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                       Local
                                                                                                             tgatcgctcaccgcgcgtgcacacggggggggccccaccagtgccccgagtgcggga 130
                                      agogotttaccaataagocotatotgacttogcacoggogcatocacacoggogagaago 190
AGAGCTTCATCCGCAAGCACCACCTCCTGGAACACCGGCGCATCCACACAGGCGAGCGGC 90059
                                                                                                                                                                                                                                                                168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 66% of reads Chemistry: Dye-terminator Big Dye; 34% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 159790 bases at least Q40 Consensus quality: 160407 bases at least Q30 Consensus quality: 160877 bases at least Q20 Consensus quality: 160877 bases at least Q20
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Insert size: 162070; sum-of-contigs
                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  44044 a
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4791. .12657
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96970. .162570
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/chromosome="7"
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1462: gap of unknown length
4690: contig of 3228 bp in length
4790: gap of unknown length
12657: contig of 7867 bp in length
12757: gap of unknown length
12757: gap of unknown length
44491: contig of 31734 bp in length
96869: contig of 52278 bp in length
162570: contig of 65601 bp in length
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70.3%;
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Pred. No. 5.5e-14;
0; Mismatches 71
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ggaagcgctttaccaataagccctatctgacttcgcaccggcgcatccacaccggcgaga 187
                                                       ACTTGACCAAGCACCAGCGCACACACACGGGCGAGCGGCCTTACAAGTGCCTAGTCTGTG 1115
                                                                                 acttgatcgctcaccgcgcgtgcacacggggcgagcggccccaccagtgccccgagtgcg 127
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Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can the complete sequences in vitro
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/product="KIAA05483.1"
/db_xref="G1:3043638"
/db_xref="G1:3043638"
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PYPCPECGKRFSQSSSLVIHRRTHSGERPYACTQCGKRFNNSSHFSAHRRTHTGEKPY
TCPACGRGFRRGTDLHKHQRTHMGAGSLPTLQPVAPGGPGAKA"
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/clone_lib="pBluescriptII
/sex="male"
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/db_xref="taxon:9606"
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Pred. No. 7.6e-13;
0; Mismatches 143;
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/rpt_family="Alu" 1595. .1862
                                                                                                                       /rpt_family="Alu"
575. .882
                                                                                                                                                                               /clone="RPCI-11_127I20" complement(41. .330)
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                    /rpt_family="Alu"
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complement(20808. 21104) /rpt_family="Alu"	errenc exon, tralle	.19559)	/*FC_***********************************	/*PC_ramity = 5.0 complement(1851818917) /rot familto "ali"	/+bc_ramily= 6.40 complement(1842018718) /rot family="8410"	16559. 1683 1150 16559. 1683 1150	/rpt_idml1y="Li" complement(1619216347) /rpt_family="all"	/rpt_ramily="Ald" complement(16083 .16185)	/16	/IPC_IGMIIY="AIU" 1506115366	complement(1440114696)	/*PC_remity	/+ptramity = niu 13761. 14148 /rnt family = nliv	/:pc_ramity = 6:10 13420: 13725 /rot formily="%):"	/+[v_ramity]	/ipc_idminiy="Alu" 12643. 13073 /rnt family="Alii"	/IPC_IAMILY="ALU" 128212576 /************************************	/*PC_remitry	11580. 11780. 11580. 11780. 1280. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580. 1580.	complement(1080110977) /rpt family="Ali;"		· I	97029987 /rot family="Ali;"	9515. 9812 /rpt family="Alu"	93949682 /rpt family="Alu"	88089139 /rpt_familv="Alu"	79318385 /rpt_family="Alu"	.7776 family-"Alu"	<pre>complement(68486983) /note="GRAIL 2 excellent exon, frame 1"</pre>	57496045 /rpt_family="Alu"	48265155 /rpt_family="Alu"	fa.	/rpt_family="Alu" /rpt_family="Alu" 4198	y="Alu"	.3504 family="Alu"	/rpt_family="Alu"
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Assembly program: XGAP4; version 4.5 sequencing vector: M13; M77815; 25% of reads Sequencing vector: plasmid; L08752; 74% of reads Chemistry: Dye-terminator ET-amersham; 0% of reads Chemistry: Dye-terminator B1g Dye; 94% of reads Chemistry: Dye-terminator B1g Dye; 94% of reads Chemistry: Dye-primer-amersham; 2% of reads Chemistry: Dye-primer B1g Dye; 1% of reads Consensus quality: 136114 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Aug 14, 2000 this sequence version replaced gi:9588436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 1 cl
                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
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Direct Submission
                                                                                                                                                                                                                            Center project name: dJ599G15
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                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
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Eutheria; Primates;
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Pred. No. 2.1e-13;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  15 cgaccgcccttccagtgtgcctgttgtggcaagcgcttccggccacaagcccaacttgat 74
                          cccgtgcaaagagtgcggccgccgcttccggcacaaaccccaacctgctgtctcacagcaa 254
                                                                                                           ctttaccaataagccctatctgacttcgcaccggcgcatccacaccggcgagaagcccta 194
CCCGTGCCCCGAGTGCGGCGAGGCCTTCAGCCTCAGCTCGCATCTGTTGAGCCACCGGCG 94094
                                                                                                                                                                                             cyctcaccyccycytycacacygycyaycygycccaccaytyccccyaytycygyaaycy 134
                                                                                  CTTCAGCTGGCGCGCCGACCTGCTCAAGCACCGGCGCCCTGCACACGGGCGAGAAGCCCTA 94154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 137778; sum-of-contigs
Insert size: 126614; 2.3% error; agarose-fp
Quality coverage: 6.30x in Q20 bases; sum-of-contigs Quality
coverage: 8.38x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 137176 bases at least Consensus quality: 137544 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15997 16096: gap of 100 bp 16097 19055: contig of 2959 bp in length 19056 19155: gap of 100 bp 19156 22087: contig of 2932 bp in length 22088 22187: gap of 100 bp 22188 29998: contig of 7811 bp in length 29999 30098: gap of 100 bp 138778: contig of 108180 bp in length 30099 138778: contig of 108180 bp in length
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8021 8120: gap of 100 bp
8121 15996: contig of 7876 bp in length
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22188. .29998
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30099. .138278
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fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-4"
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/db_xref="taxon:9606"
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Pred. No. 4.8e-13;
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                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
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ORGANISM
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K.,

Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,

Funke,R., Gage,D., Galagan,J., Gaddyna,S., Gilbert,D., Grant,G.,

Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,

Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,

Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,

Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Baylin,B.,

Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,

Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,

Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gattcacaagcgatccgaggggtcggcccaggccgcccccggccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (08-MAY-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 24, 2000 this sequence version replaced gi:8516078. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 29802)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus chromosome, clone CT7-345D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE2
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                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that h
                                                                                                                                                                                                                                        by the finished sequence as soon as it is available and the accession number will be preserved.

1 29802: contig of 29802 bp in length.
                                                                                                                                                                                                                                                                                                                                        provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project Information Center project name: L738 Center clone name: 345_D_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center
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                             /clone_lib="CitbCJ7 Mouse BAC"
6618 c 6969 g 8161 t
                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                       clone="CT7-345D4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29802 bp DNA HTG sclone CT7-345D4, *** SEQUENCING
                                                                                                                                                                                       .29802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                      estimates that have
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ROGRESS ***,
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Best Local Similarity
Matches 197; Conserv
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                                                                                                                                                                                                              On May 30, 2000 this sequence version replaced gi:7249370 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                       Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC015887 201458 bp DNA HTG 30-MAY-2000 Mus musculus clone CT7-315E6, WORKING DRAFT SEQUENCE, 20 unordered
                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Contact: sequence_submissions@genome.wi.mit.edu
                                 Web site: http://www-seq.wi.mit.edu
                                                                       Center code: WIBR
                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
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Pred. No. 1.6e-12;
"" smatches 112;
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Sequencing vector: Plasmid; n/a; %-0.f%% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
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5931: gap of 100 bp
7380: contin ~ 7380
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61254: contig of 16283 bp in
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18405: contig of 3111 k
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20293: contig of 1788 k
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44871: contig
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2600: contig of 1440 bp in length
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183; Conservative
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Pred. No. 1.5e-12;
0; Mismatches 110;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                                                              Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Cent Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
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/tissue_type="colon"
/note="cloning vector pME18SFL3"
1. .2878
                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COL09895"
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fis, clone COL09895, highly similar to
for AP4 zinc finger protein.
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Suzuki,Y., Obayashi,M., Nishi,T.,
ra,Y., Isogai,T. and Sugano,S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Mikrobiologie und Hygiene, Universitaet Regensburg, Franz-Josef-Strauss-Aliee 11, 93053 Regensburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1
Dobner, T.G.
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AJ245553
AJ245553.1 GI:574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dobner, T.G., Fischer, M. and Groitl, P. Cloning of a novel zinc finger protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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1 (bases 1 to 2878)
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                                                                                                                                                                /product _ AP4 protein  
/product _ AP4 protein  
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/protein_id="CAB53100.1"
/protein_id="CAB53100.1"
/db_xref="GI:5748565"
/dref="GI:5748565"
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/dref="GI:5748565"
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/d
                      TCAECGKNFGKKTHLVAHSRVHSGERPFACEECGRRFSQGSHLAAHRRDHAPDRPFVC
PDCGKAFRHKPYLAAHRRIHTGEKPYVCPDCGKAFRQKSNLVSHRRIHTGERSYACPD
CDRSPSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV"
1973 c 839 g 538 t
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                                                                                                                                                   <u>AVPLKPAQEPPPGAPPEHPQDPIEAPPSLYSCDDCGRSFRLERFLRAHQRQHTGERPF</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AP4"
106. .1776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="zinc finger protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AP4"
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for AP4 zinc finger protein.
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                 cyatccgagggtcggcccaggccgccccgggcccggggagcccccagctgccagccggc 60
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Homo sapiens (
AF201303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-NOV-1999) Pathology, University of Vermont, Medical Alumni Building, Burlington, VT 05405, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The dhfr oribeta-binding protein RIP60 contains 15 zinc fingers: DNA binding and looping by the central three fingers and an associated proline-rich region succeed Acids Res. 28 (2), 570-581 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 28
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                                                                                       Similarity
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                                                                      Conservative
                                                                                                                                                                                                                                                                                                      /protein_id="AAF26712:1"
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HRQVHAAATPDLGFACHLCGQSSRGWVALVLHLLAHSAAKQPTACPKCERRFWRRKQL
RAHLRRCHPPAPEARPFICGNCGRRFAQWDQLVAHKRVHVAEALEEAAAKALGPRPRG
RAHLRRCHPPAPEARPFICGNCGKRFKHKPNLIAHRRVHTGERPHQCPECGKRFTNK
                                                                                                                                                                                                                                                      PYLTSHRRIHTGEKPYPCKECGRRFRHKPNLLSHSKIHKRSEGSAQAAPGPGSPQLPA
GPQESAAEPTPAVPLKPAQEPPPGAPPEHPQDPIEAPPSLYSCDDCGRSFRLERFLRA
HQRHDTGERPFTCAECGKNFGKKTHLVAHSPVHSGERPFACEECGRRFSQGSHLAAHR
                                                                                                                                                                                                                     {	t HTGERPYACPDCDRSFSQKSNLITHRKSHIRDGAFCCAICGQTFDDEERLLAHQKKHD}
                                                                                                                                                                                                                                       PDHAPDRPFVCPDCGKAFRHKPYLARHRRIHTGEKPYVCPDCGKAFSQKSNLVSHRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HeLa"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="dhfr oribeta-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains 15 C2H2-Kruppel-like zinc fingers"
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RIP60 mRNA, complete cds.
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AC005586
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Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99033792
                                                                                                                                                                                                         Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington Submitted (2000) Of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 132150)
Stoneking,T., Ozersky,P., Wohldmann,P.
The sequence of Homo sapiens PAC clone
                                                                                                      Submitted (30-SEP-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Jun 12, 2000 this sequence version replaced g1:3907529.
                                                                                                                                                                                                                                                               4 (bases 1 to 132150) Waterston, R.H.
                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (01-SEP-1998) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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HTG.
                                                                                                                                                       Direct Submission
                                                                                                                                                                    Waterston, R
                                                                                                                                                                                                    MO 63108,
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                                                                                                                                                                                     (bases 1
            Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
Center project name: H_DJ0584D14
                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                          ---- Genome Center
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RP4-584D14 from
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                                                                                                                                                                                                                                                                                                          Sequencing Center, Washington 4444 Forest Park Parkway, St.
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RP4-584D14
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                                                                                                                                                                                                                                                                                                             Louis,
                                                                                                                         USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of convencing collaboration between the NHGRI Chromosome **7** a mapping Mapping and

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence RP4-584D14 from base position 21655 to Trich. This region was sized with PCR from genomic D hindili digest with band size 3643 real, and 3642 in sequence RP4-584D14 from base position 22628 to 2263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the right is RP5-820A21, 200 base pair overlap. Actual start of this clone is at base position 1 of RP4-584D14; actual end is at base position 131954 of RP4-584D14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one male donor.
The clone may be obtained either from Genome Systems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represented by sequence derived by PCR Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.genomesystems.com) or Research Genetics, Inc.
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/db_xref="taxon:9606"
/chromosome="7"
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_family="MER4-group"
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/note="similar to Oryctolagus cuniculus EST C83534 (NID:g3062491)"
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8591. .9167
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8459. .8461
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8075. .8451
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8008. .8309
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8707. .8845
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/rpt_family="Alu"
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7976. .8575
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/note="match to
7886. .8357
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/note="similar to
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VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6910757. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donneil, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
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HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L.,
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                                                                                                                                                                                                                    NOTE: This record contains 174 individual sequencing reads that have not been assembled into contigs. Runs of Nare used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                        overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                     However,
                                                                                                                                                 will be sequenced to completion. In
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                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                       Center clone name:
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Eutheria;
944: gap of 100 bp
1799: contig of 855 bp in length
1899: gap of 100 bp
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Primates;
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7 23040: cont
1 23140: gap of
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3771:
3871: gap
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12520: gap of 100 bp
13422: contig of 902 bp in
13522: gap of 100 bp
14382: contig of 860 bp in
 36578: contig of 875
36678: gap of 100 b
37519: contig of 841
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11578: gap of 100
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7016: gap of 100 bp
27891: contig of 875 b
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28859: contig of 868 bp
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (22-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 25, 2000 this sequence version replaced gi:8468712.
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                                                                                                               Center project name: HAVI
Center clone name: RP11-665J20
Center clone name: RP11-665J20
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 208190 bases at least Q40
Consensus quality: 224572 bases at least Q20
Consensus quality: 231987 bases at least Q20
Estimated insert size: 219523; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 5.8x in Q20 bases; sum-of-contigs estimation
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Query Match

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* sequencing reads that have not been assembled into * contigs. Runs of N are used to separate the reads * and the order in which they appear is completely

NOTE: This record contains 72 individual

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G. Campopiano, A., Castle, A., Chepel, Y. Colangelo, W. Castle, A., Chepel, W. Colangelo, W. Colangelo, W. Castle, A., Chepel, W. Colangelo, W. Colangelo, W. Castle, A., Chepel, W. Colangelo, W. Castle, W. Colangelo, W. Castle, A., Chepel, W. Chepel, W. Colangelo, W. Chepel, W. Colangelo, W. Chepel, W.
                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-APR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 21, 2000 this sequence version replaced gi:7417761 All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EukaryOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC034263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodge,S., Domino,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roung, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vassiliev,H., Viel,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC034263.2 GI:7960368
NOTE: This record contains 158 individual sequencing reads that have not been assem contigs. Runs of N are used to separate t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 131602)
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                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center code: WIBR
                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F.A. & Green, P. (1996-1997)
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                                                                                                                                             clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doyle, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ferreira, P., FitzHugh, W., Gage, D.,
been assembled into separate the reads
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                                                                                                                                                                                                                                                                                                                                                            Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ye, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                 100 bp 1 18748 | contig of 758 bp in 18749 | 18848 | gap of | 100 bp in 9621 | 19720 | gap of | 100 bp in 9621 | 19720 | gap of | 100 bp in 9621 | 19720 | gap of | 100 bp in 162 | 20561 | gap of | 100 bp in 163 | 2131 | contig of 770 bp in 16 | 132 | 2141 | gap of | 100 bp | 100 bp
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100 b<sub>1</sub>
2/290: contig of 759 b
11 27390: gap of 100 hr
1 28142: conti
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10 15419: gap of 100 bp

10 16181: contig of 762 b

2 16281: gap of 100 bp

2 17038: contig of 757 b

2 17138: gap of 100 bp
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6744:
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26431: contig of 751 bp
26531: gap of 100 bp
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100 bp
17890: contig of 752 bp ii
7990: gap of 100 hm
18748: con++-
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14458: contig of 745 bp
1558: gap of
15319: cc.
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9293:
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8439:
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4191:
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3331:
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of 100 bp
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54597: contig of 741 bp in
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54697: contig of 750 bp in
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52173; contig of 746 bp in
52173; gap of 100 bp
52897; contig of 724 bp in
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40969: contig of 746 bp in length
41069: gap of 100 bp
41825: contig of 756 bp in length
42574: contig of 756 bp in length
42574: gap of 100 bp
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42774: gap of 100 bp
43517: contig of 743 bp in length
43617: gap of 100 bp
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38406: contig of 760 bp i

8506: gap of 100 bp

39273: contig of 767 bp i

9373: gap of 100 bp

40123: contig of 750 bp i
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52897: 7
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5044: gap of 100 bp
35820: contig of 776 bp i
5920: gap of 100 bp
36680: contig of 760 bp i
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53756: contig of 759
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30688: contig of 756 bp
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31558: contig of 770 bp
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132: gap of 100 bp
30688: contig of 756 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (03-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUL 13, 2000 this sequence version replaced gi:6513976. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baddwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forrestra, P., FitzHugh, W., Forrest, C., Fuke, R., Gage, D., Galgan, T., Gardy, B., Frant G., Gardy, B., Gard
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                                     NOTE: This record contains 81 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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Center clone name: 20_M_3
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Colney, Norwich, No
Notes:
Streptomyces coelic
                                                                                                                          are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codons.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
http://www.nih.go.jp/
http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the
correct initiation codon. Where possible we choose an initiation
codon (atg, gtg, ttg or (att)) which is preceded by an upstream
ribosome binding site sequence (optimally 5-13bp before the
                                                                                                                                                                                                                                                                                                                                                                                               available on the World Wide Web. (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-FEB-2000) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A E-mail: barrellesanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by the BBSRC and Details of S.
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Streptomyces coelicolor A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
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A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 8058)
Redenbach, M., Kieser, H.M.,
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<u>:</u>

/product="hypothetical protein SCE56.03c"

/note="SCE56.03c,

len:

260

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small overlap between neighbouring submissions.
Cosmid E56 Overlaps cosmid E59 on the AseI-E ge
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IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                   /translation="MRYIRLGTTGLEVSAIALGCMGFGEPDRGGEPWSLGADPSRDII
RQALEGGVNFLDTANGYSAGNSEEIVGAVKDPARREEVVLSTKVWMRKRPGPWGAGL
SRKAIFAELDASLKRLGTDYIDLYGLIRWDVDTPIEFCTLEALHDVVKSGKVRVLGASS
MYAWQFAKALYLADLNGWTRFVSMQDHYNLIHREAEREMLPLCADQGIGVIPWSPLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coelicolor putative aldo/keto reductase (fragment) SCF81.28c, 307 aa; fasta scores: opt: 1370 z-score: 1572.6 E(): 0; 65.2% identity in 305 aa compared to SW:NORA_ASPFL (EMBL:U32377) Aspergillus flavus norsolorinic acid reductase (EC 1.1.1.-) NorA, 388 aa; fasta scores: opt: 572 z-score: 659.1 E(): 2.7e-29; 32.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"SCE56.02, possible oxidoreductase, len: 336 similar to TR:CAB61562 (EMBL:ALI33171) Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SCE56.02"
904. .1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTVPEPRDTDVAAPVEPALAPAAPAETVLSRAYRALSIGIVSVI
VLIAFEATAVGTAMPVAARELDGVSLYAFAFSGYFTTSLFGMVLSGQWSDRRGPLAPL
TTGIATFAAGLVLSGTAGAMMLFILGRAVQGFGGGLVIVALYVVVGRAYPERLRPAIM
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                                                               complement(1881
/gene="SCE56.03c"
/note="scrrc ?-
                                                                                                                                                                                          VVTSPIVGVTKPAQLADAIAAVDVGLDEDEAAYLEEPYQPHEAAYLEESFYKARPAAA
                                                                                                                                                                                                                            GRLTRARDTATARAGTDEGGRILYRDEDQAVAERVREIAGRRGLSPAQVALAWVMRNP
                                                                                                                                                                                                                                                                                                                                                                                  /product="putative oxidoreductase"
/protein_id="CAB72221.1"
/db_xref="GI:6912006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fasta scores: opt: 572 z-sc
identity in 329 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAFAAGWVVPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative transport protein (partial)"
/protein_id="CAB72220.1"
/db_xref="GI:6912005"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptomyces
/strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid E56"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SCE56.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCE56.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCE56.01c, possible transport protein (partial),
len: >170 aa; similar to Tr:AAF11647 (EMBL:AE002045)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCE56.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /partia
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complement(1..513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                            5.03c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
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DFSQAAQASRAEADAAAARQASGQDVTGQWSIPVADGDLPDESGEFTTSSLAEQW
GTGAPATLPGGAPAPWATQPAGQPWGEDAPRGPGAPGAPATGPGA
GTGAPATLPGGAPAPWATQPAGQPWGEDAPRGPGAPGAPGAPATGPGA
GEGHADAGHARADALLSGYGGGHUSGADAGHGPDAAVGPHGFGFSAPGARPVPHAHGP
STASGPGEGHGPGPAASVHGHDPAVSPDGPRADGSYAHAPGVDTQSAAGAAGAAGAGGG
KAPDGAAPGGSGTATDGPRGAEEAPEGPAGRSAGPHEEARAGSPREAPAGPVTDRAPTA
GRERAPEPAGEHGQAPEGEPRPESPAAPQGVPADADSDRADSPDPADPTDPTG
RGTDAADAGSGADGPEAVTDGVPDAAQGPSAPAGGDBHPLASYVLRVRGADRPVTDA
WIGESLLYVLBERLGLAGAKOGCSQGEGGACNVQVDGRLVASCLVPSYTAAGSEVRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5075..7396)
/gene="SCE56.05c"
/gene="SCE56.05c unknown, len: 773 aa. High content in proline, glycine and alanine. Contains Pfam matches to entries PF00111 fer2, 2Fe-25 iron-sulfur cluster binding domains and PF01799 fer2_2, [2Fe-25] binding domain and match to Prosite entry PS00197 2Fe-25 ferredoxins, iron-sulfur binding region signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SCE56.04c, possible oxidoreductase, len: 773 aa; similar to TR:Q92BN7 (EMBL:AL034492) Streptomyces coelicolor putative oxidoreductase SC65.08, 828 aa; fast scores: opt: 1088 z-score: 1144.8 E(): 0; 42.2% identity 1782 aa overlap and to SW:XDH_DROPS (EMBL:M33977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE56.04c"
/note="SCE56.04c, possib
similar to mn ^^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF01315 Ald_Xan_dh_C, Aldehyde oxidase and xanthine dehydrogenase, C terminus, score 279.60, E-value 3.9e-80" complement(5075. .7396) /gene="SCE56.05c" complement(5075. .7396)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LARQIVQDTLGVDEVQVAPVDTDQPPAGPGCRGRHTWYSGGAVERAAKMYRTQLLQPL
AHQFGMSTELLQIADGKITSYDGVLSTTVTEALDGKELMATAQCRPHPTEPLDEAGQG
DAFVGMAFCAIRAVVDVDIEIGSVRVVELAVAQDVGRVLNPAQLTARIEAGVTQGVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGQADRPVFASEAVRHHGEPLAAVAADHPDTARMAAAAVIVEYELLDPVTDPEQAFEA
EPLHPDGNLIRHIPLRHGDPDAAGEIVVEGLYRIGRQDPAPIGAEAGLAVPRPDGGVE
LYLASTDPHGDRDIAAACYGLSPEQVKIVVTGVPGATADREDQGFQLPLGLLALKTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila pseudoobscura xanthine dehydrogenase (EC 1.1.1.204) Xdh, 1342 aa; fasta scores: opt: 517 z-score: 540.4 E(): 1.1e-22; 27.4% identity in 762 aa overlap. Contains Pfam match to entry PF01315 Ald_Xan_dh_C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="SCE56.04c"
complement/??-
                                                                                                                                                                                                                                                                                                                                      /translation="MTDDQHGDPHGDQHGQGTPPGGSRWDPLPQGDYDDGATAFYKLP
EGGVDALLASSDSPLAAPGHGYVPPQITVAPATTAGTDPAATGSWAAPSAPSAPVDGT
QWQVPDAGQDPAAHQGYGGYPAQQDPYGGAAPYDVHAGQGAPGHDDRFAYQPGPTGQW
                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein SCE56.05c"
/protein_id="CAB72224.1"
/db_xref="GI:6912009"
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ASPAAVASAVRAATGRPVNRLPIRPQAAVATGH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWKLTATREESFLGHTHRHPTLLRYRHHADABGRIVKVEAQILLDAGAYADTSSDALA
AAVAFAGPYVVPNAFIEGWAVRTNNPPSGHVRGEAMQVCAAXEAQMOKVAKKLGLD
PABWRLRNVLATGDVLPTGOTVTCFAAPVAELLAAVRDFPLPALPKDTPDEDWLLFGGE
EGAGEPGAVRRGVGYGIGMVHMLGAEGADEVSTATVKVQGGVATVLCAAVETGQGFTT
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FPYAADLWAEGLLWAAVLRSPHPRARIVSIDTTHAREMPGVRAVVTHEDVPGSPLHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative oxidoreductase"
/protein_id="CAB72223.1"
/db_xref="gI:6912008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="Myarslrrsanosrrhadghtfsgeethhaydfggttitrgaaadu
RTavPSLVTRVRLATVYEDPARTRDAARRPQASGERSJUWTSTLMSCLLLAVSHRAE
PGTSRDLPPRFLDREFGRHRVTRFEDIDFPRPLTHEDTRFLXETGLLEBDARPFRLD
DDLPLPTLAEYCEEHPDQPVPPGADHLVRLGRLADGAHVAVDGTTGAVLTWRTPDGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPLVSDVSALALTLWALRRAGRLETSAGGGPDYREAAAGRAL"
complement(2757...5078)
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/db_xref="GI:6912007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCE56.04c"
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/transl_table=11
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RESULT 11
AP001052/c
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KEYWORDS
                                                   FEATURES
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Best Local S
Matches 87
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Best Local
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caggggccccgccagagcacccgcaggaccccgatcgaagccccccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agcacccgcaggacccgatcgaagccccc 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agcccaccccggcggtacctctgaaaccggcccaggagccgccgccaggggccccgccag 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aggccgccccgggcgggagcccccagctgccagccggccccccaggagtccgcggccc
                                                                               aggagtccgcggccgagcccaccccggcggtacctctgaaaccggcccaggagccgccgc 124
                                                                                                                                               ccgaggggtcggccaggccgcccgggcccggggagccccagctgccagccggcccc
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87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 145540)
Shimizu, N., Kudoh, J. and Shibuya, K.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax:81-3-3351-2370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular
Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan
(E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens genomic DNA, chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145540)
Shimizu, N., Kudoh, J. and Shibuya, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens pre-pro-B cell cell_line:FLEB14-14 DNA, clone_lib:Keio
BAC library clone:KB22A5.
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                              /clone="KB22A5"
/clone_lib="Keio BAC library"
36783 c 36979 g 35786 t
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                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .145540
                                                                                                                                                                                                                                                                                                                                   /cell_type="pre-pro-B cell"
/chromosome="21"
                                                                                                                                                                                                                                                                                                                                                                   /cell_line="FLEB14-14"
                                                                                                                                                                                                  27.8%;
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                                                                                                                                                                                    0;
                                                                                                                                                                                Score 49.2; DB 48;
Pred. No. 3.5;
0; Mismatches 73;
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* Innestrasse 73, D-14195 Berlin, Germany,

* e.mail: info-chr21@molgen.mpg.de

* URL: http://chr21.rz-berlin.mpg.de/

AL163297: Submitted (10-Apr-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic Sciences Center, Human Genome Research Group * Institute of Molecular Biotechnology, Genome Analysis * Keio University School of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome Analysis * Max-Planck Institute for Molecular Genetics (addresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hattori, M., Fujiyama, A., Taylor, T.D., Watanabe, H., Yada, T., Park, H.S., Toyoda, A., Ishi, K., Totoki, Y., Choi, D.K., Soeda, E., Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K., Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R., Patterson, D., Reichwald, K., Rump, A., Schillhabel, M., Schudy, A., Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K., Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S., Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G., Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A., Reichelt, J., Kauer, G., Bloccker, H., Ramser, J., Beck, A., Klages, S., Hennig, S., Riesselmann, L., Dagand, E., Wehrmaeyer, S., Borzym, K., Gardiner, K., Nizetic, D., Francis, F., Lehrach, H., Reinhardt, R. and
                                                                                                                                                                                                                                                                        160-8582, Japan,
* e.mail: nshimi
* URL: http://ww
                                                                                                                                                                                                                                                                                                                                                                                                                  * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 30, 2000 this sequence version replaced gi:7717416. The chromosome 21 mapping and sequencing consortium consisting *RIKEN Genomic Sciences Center, Human Genome Research Group, *Sagamihara 228-8555, Japan,
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                                                                                                                                                                     * GBF, Dept. of Gen
* Mascheroder Weg
info.genome@gbf.de
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Nature 405 (6784), 311-319 (2000)
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AP001752.1 GI:7768757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.mail: hattori@gsc.riken.go.jp
URL: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                             Keio University School of Medicine, Molecular Biology,
                                                                                                                                                                                                                                                                                                                                                                                           URL: http://genome.imb-jena.de/
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                                                                                                                                                                                                                                                                 il: nshimizu@dmb-med.keio.ac.jp
http://www.dmb.med.keio.ac.jp/
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                                                                                                                                                                                            1, D-38124 Braunschweig, Germany,
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K., Soeda,E.,
                                                                                                                                                                                              * e.mail:
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                                                                                                                                                                                                                                          note="MLT1E2"
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/organism="Homo sapiens"
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                                                                                                                                               5 ccgaggggtcggcccaggccgccccgggggagcccccagctgccagccggcccc 64
                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                            /rpt_type=DISPERSED 12274. .12590
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complement(7441.
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ILNGEVLESFQKLKIVEKNLERKEQELEQLKMDCEHFKARLETVQADNIREKKEKLAL
RQQLNEAKQQLLQQAEYCTEMGAAACTLLWGVSSSEEVVKAILGGDKALKFFSITGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(<7441. .7566,23941. .24073,26891. .27040,
37908. .38011,50206. .50356,51680. .51715))
                                                                                                                                                                                                                                                                                                                                                         /rpt_type=DISPERSED
12004. .12273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="LTR/MaLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAA95539.1"
/db_xref="GI:7768758"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HSF2BP"
                                                                                                                                                                                                                                                                                                                  rpt_family-"LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="SINE/Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="DNA/MER2_type"
/rpt_type=DISPERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family-"SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluJo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HSF2BP"
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                                                                                                                                                                                                 Score 49.2; DB Pred. No. 2.3; 0; Mismatches
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                                                                                                                                                     * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                NOTE: This record contains 74 individual
                                                                                                                                       the record is updated, the accession number will
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                                                                                                                     preserved.
                    1 793: contig of 793 bp in length
794 893: gap of 100 bp
1788 2572: contig of 785 bp in length
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---- Genome Center

2572: contig of 2672: gap of 10

100 bp of 794 bp in length 100 bp of 785 bp in length

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Anderson, S., Baldwin, J., Barma, N., Beda, F., Boguslavkly, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M.,
Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-pierre, N., Grantt, G., Hagos, B., Heaford, A., Horton, L.,
Grand-pierre, N., Grantt, G., Hagos, B., Heaford, A., Horton, L.,
Kiein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Kiein, J., Landers, T., McKernan, K., McCheeters, R., Meidrim, J.,
McEwan, P., McGurk, A., McKernan, K., McCheeters, R., Meidrim, J.,
Mcman, C.H., O'Connor, T., O'Donnell, P., O Neil, D., Olivar, T.M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
W.X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
Submitted (28-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 65523)
Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC024266.1 GI:7107792
HTG; HTGS_PHASE0.
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                                                                                                                                                                                       Direct Submission
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caccccggcggtacctctgaaaccggcccaggagccgccgccaggggccccgccagagca 143
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                                  88; Conservative
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47014 47792: contig
47793 47892: go of
47793 47892: go of
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21 53220: gap of 10:
21 53973: contig of 75:
4 54073: gap of 100
4 54862: contig of 76:
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2 58451: contig of 7

32 58551: gap of 9

32 59333: contig of 7

34 59433: gap of 10

34 60245: contig of 8
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36370: cr
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56760: gap of 100 bp
57571: contig of 811 bp
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52227: contig of 826 bp
52327: gap of 100 bp
53120: contig of 793 bp
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45162: contig of 743
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44319: contig
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38157: con
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334: gap of 1
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43390: contig of 793
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12497: contig of 803
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contig of 741 bp i
ap of 100 bp
contig of 772 bp i
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0 15979: gap of 10 6 1645: contig of 10 6 16845: gap of 10 6 17645: contig of 10 6 17745: gap of 10 6 18541: contig of 10 2 18641: gap of 10

100 bp

800

bp in length

100 bp 796 bp in

7.9836: gap of 100
7.10619: contig of 7
1010719: gap of 10
11503: contig of 7
14.11603: gap of 10
12326: contig of 7
7.12426: gap of 10
7.13201: contig of 7
13201: contig of 7
13201: gap of 10
2.13301: gap of 10

100 bp 723 bp in

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contig of contig of

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9 31928: contig o.
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length length length length 65 22164: gap of 100 bp
65 22935: contig of 771 bp in le
65 22935: contig of 771 bp in le
65 23951: gap of 100 bp
36 23851: gap of 100 bp
36 23851: gap of 100 bp
52 24827: contig of 816 bp in le
52 24927: gap of 710 bp in le
62 24927: gap of 100 bp
63 25698: contig of 778 bp in le
64 26568: gap of 100 bp
67 26586: contig of 788 bp in le
68 26686: gap of 100 bp
68 27505: contig of 819 bp in le
68 26686: gap of 100 bp
68 27505: gap of 100 bp
68 27605: gap of 100 bp
69 25781: gap of 100 bp
60 27605: gap of 100 bp
61 27505: contig of 819 bp in le
62 27605: gap of 100 bp
63 28408: contig of 803 bp in le
64 28508: contig of 803 bp in le

7 20476: gap of 10 7 21179: contig of 7 0 21279: gap of 10 0 22064: contig of

100 bp £ 785 bp in length

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100 bp in 1 g of 806 bp in 1 100 bp g of 829 bp in 1 100 bp g of 703 bp in 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jul 13, 2000 this sequence version replaced gi:6921662. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, S., Baldwin, J., Barna, I
Boguslavkiy, L., Boukhgalter, B.,
Choepel, Y., Colangelo, M., Collin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (07-FEB-2000) Whitel Research, 320 Charles Street,
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Submitted (07-FBB-2000) Whitehead Institute/WIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.
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                                                                                                                                                                                                                                              sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                      However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This record contains 83 individual
                                                                                                                                                                                     the record
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L6502
Center clone name: 565_K_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
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                                                                                of 779 bp in length
100 bp
of 767 bp in length
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5179:
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26111: contig
26211: gap of
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22629: contig of 749 bp
22729: gap of 100 bp
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15668:
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90 58489: gap of 100 bp
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76 60275: gap of 100 bp
76 61057: contig of 782 bp in length
58 61157: gap of 100 bp
58 61927: contig of 770 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49570: contig of 750 bp i
71 49670: gap of 100 bp
11 50454: contig of 784 bp ii
5 50554: gap of 100 km
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 37540: gap of 100 bp
41 38296: contig of 756 bp
97 38396: gap of 100 bp
97 39363: contig of 767 bp
64 39263: gap of 100 bp
64 40040: contig of 777 bp
64 40140: gap of 100 bp
65 41014: gap of 774 bp
15 41014: gap of 100 bp
16 41014: gap of 774 bp
17 41014: gap of 774 bp
18 41014: contig of 774 bp
18 41014: gap of 100 bp
18 41014: gap of 787 bp
                                                                                                                                                                                                                                                                                                                                                                                61057:
3 61157: ar-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35707: contig
35807: gap of
                                                                                                                                                                                                                                                                           27.6%;
52.0%;
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contig of 767
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contig of 774 bp in
                                                                                                                                                                                                                                                                    Score 48.8;
Pred. No. 5.
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100 bp in )
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1777 bp in )
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REFERENCE
AUTHORS
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KEYWORDS
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AC027375/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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AC027375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye, Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatord, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McGarthy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (30-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-7E17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campopiano, A., Castle, A., Choepei, Y., Colangeio, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boguslavkiy,L., bounny,
Boguslavkiy,L., Castle,A.,
De
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASEO
                                                                                                                                                                sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                     be preserved.
                                                                                                                                          will be sequenced to completion. In
                                                                                                                                                                                                                                                                                                                                                         NOTE: This record contains 80 individual
                                                                                                                 the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 68581)
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                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: L5319
Center clone name: 7_E_17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- Genome Center
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Eutheria; Primates;
                                      820:
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720: contig of 720 bp in length gap of 100 bp 1593: contig of 773 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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clone RP11-7E17 ma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                               the event
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LOW-PASS SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research
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1693: gap 2467:

yap of lu 2467: contig of : gap of v331.

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3431:

gap of

4207 3331

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9401: contig of 01: gap of 10274: contig of

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7766: 6916:

7666: contig of 66: gap of 10 8540: contig of 10: gap of 10

6029:

6816:

contig of contig of contig of contig of contig of

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5929:

5 10374: gap of 10 11122: contig of 7 11122: gap of 10 11969: contig of 7

13794:

gap of 1 68: contig of gap of 1

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of 750 bp in length
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64 4635: gap of 100 bp
96 46495: gap of 100 bp
96 47248: contig of 753 b)
96 49 47348: gap of 100 bp
97 48118: contig of 770 b)
119 48218: gap of 100 bp
119 48218: gap of 100 bp
119 48976: contig of 758 b)
129 49834: contig of 758 b)
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136 50692: contig of 758 b)
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31070

70: gap of 31839: contig of

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2306 22405

21542: 20668:

gap of 100 05: contig of 763

100 bp

4890 24989

1 24140:

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19ap of 174 b

100 bp f 778 bp

100 bp f 757 bf

23262:

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763 772

18926: 18054:

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759

17195:

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719 100 bp

16376: 15522: 14668:

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Search completed: February 22, 2001, 03:12:23 Job time: 14801 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

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	26.5	26.5	26.5	26.8	26.8	26.8	26.9	27.3	27.9	27.9	28.6	7	28.7	ū	32.3	55.1	100.0	100.0	100.0	100.0	Query Match
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Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Sugano, Institute of Medical Science, University of Tokyo,
                                                                                                                                                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, Tradition of Medical Science, Tradition of Medical Science, Traditional Medical Medical Science, Traditional Medical Me
                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Genome Structure Analysis, Human Genome (Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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2 (bases 1 to 2878)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T. and Nakamura,Y.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CCL09895"
/clone_lib="COL"
/tissue_type="colon"
/note="cloning vector pME:
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Query Match
Best Local Similarity
Matches 441; Conser
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Homo sapiens mRNA |
AJ245553
AJ245553.1 GI:5748
AP4 gene; AP4 prott
                                                                                                                                                        Submitted (17-AUG-1999) Dobner T.G., Institut fuer Medizinische Mikrobiologie und Hygiene, Universitaet Regensburg, Franz-Josef-Strauss-Allee 11, 93053 Regensburg, GERMANY
                                                                                                                                                                                                                                                                                   1 (bases 1 to 2878)
Dobner, T.G., Fischer, M.
Cloning of a novel zinc
                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                   2 (bases 1 to 2878)
Dobner, T.G.
                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Eutheria; Primates; Catarrhini; Hominid
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/gene="AP4"
106. .1776
/gene="AP4"
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AP4 zinc finger protein"
a 974 c 826 g 518 t
                                                     /cell_line="HeLa"
106. .1776
                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                            1. .2878
                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            GI:5748564
AP4 protein;
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Pred. No. 5e-62;
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P4 zinc finger protein.
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REFERENCE
AUTHORS
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AF201303
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ORIGIN
                                                                                                                                SOURCE
                                                                                                                                               KEYWORDS
                                                                                                                                                              VERSION
                                                                                                                                                                             ACCESSION
                                                                                                                                                                                        DEFINITION
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Best Local :
                                TITLE
                                                                                                                   ORGANISM
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2954)

1 (bases 7. R., Montigny, W., Zeltser, L., Dailey, L., Gilbert, J.M. a)
                                                                                                                                                                        Homo sapiens
AF201303
The dhfr oribeta-binding protein RIP60 DNA binding and looping by the central associated proline-rich region
                                                                                                              Homo sapiens
                                                                                                                                                            AF201303.1
                                                                                                                                                                                                      AF201303
                                            Heintz, N.H.
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973 c 839 g 538 t
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AVPLKRAQEPPPGAPEHPQDP LEAPESLYSCDDCGRSTRLERFAHQRQHTGERPF
TCAECGKNFGKKTHLVAHSKYHSGEREPFGCEBCGRRFSQSHLAAHRRDHAPDREPC
PDCGKAFRHKPYLAAHRRIHTGEKPYVCPDCGKAFRQKSNLVSHRRIHTGERSYACPD
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PAARPF I CGNCGRSFAQWDQLVAHKRVHVAEALEEAAAKVLGPRSRGRPAVTAPRPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MGPAQPRLLSGPSQESPQTLGKESRGLRQQGTSVAQSGAQAPGRAHRCAHCRRHFPGWVALMLHTRRCQARLPLPCPECGRRFRHAPFLALHRQVHAAATPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="AP4 protein"
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Pred. No. 5e-62;
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagtgcgggaagcgctttaccaataagccctatctgacttcgcaccggcgcatccacacc
                                                                                             ATCGAAGCCCCCCCCCTCCCTC
                                                                                                                                                                        CCTCTGAAACCGGCCCAGGAGCCGCCGCCAGGGGCCCCGCCAGAGCACCCGCCAGGACCCG
                                                                                                                                                                                          cctctgaaaccggcccaggagccgccgccaggggccccgccagagcacccgcaggacccg
                                                                                                                                                                                                                                                GGGAGCCCCAGCTGCCAGCCGGCCCCCAGGAGTCCGCGGCCGAGCCCACCCCGGCGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCCCAACTTGATCGCTCACCGCCGCGTGCACACGGGCGAGCGGCCCCCACCAGTGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houchens, C.R., Gi
Direct Submission
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Conservative
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/product="dhir oribeta-binding protein RIP60"
/protein_id="AAF26712.1"
/protein_id="AAF26712.1"
/db_xref="gi:6716714"
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/translation="MLERCREPEGWVALWLHTRCQARLPLEPGECGREFRHAPFLAL
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HRQVHAAATPDLGFACHLCGGSFRGWVALWLHLAHSAAKQDIACEEAAAKALGPRPRG
RAHTRCHPPAPEACHLCGGSCRGRFRHKPWLIAHKRVHTGERPHQCPECGKRFTNK
PRATTSHRRIHTGEKPYPCKECGRRFRHKPWLIAHKRVHTGERPHQCPECGKRFTNK
PYLTSHRRIHTGEKPYPCKECGRRFRHKPWLIAHKRYBGSAQAAFGPGSPQLPA
PYLTSHRRIHTGEKPYPCKECGRRFRHKPWLISHKKKFSGSAQAAFGPGSPQLPA
TTTTHERTHTTHERTHTGEKPYPCKECGRRFRHKPWLISHKKTSGSAQAAFGPGSPQLPA
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PDHAPDRPFVCPDCGKAFRHKPYLARHRRIHTGEKPYVCPDCGKAFSQKSNLVSHRRI
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/db_xref="taxon:9606"
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                                                                                                            Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 12, 2000 this sequence version replaced gi:3907529.
                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (01-SEP-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                     MO 63108,
5 (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stoneking, T., Ozersky, P., Wohldmann, P. and Le, T. The sequence of Homo sapiens PAC clone RP4-584D14
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Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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                                Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                             Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Center project name: H_DJ0584D14

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

101

This clone was derived from human PAC library RPCI-4, prepared Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is The library is from Institute

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2000 this sequence version replaced gi:7249370. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
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Sequencing vector: M13; M77815; 44% of reads sequencing vector: Plasmid; n/a; %-0.f% of reads 55.555555555556Chemistry: Dye-primer amersham; 58 Chemistry: Dye-terminator Big Dye; 42% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 192611 bases at least 0.0 consensus quality: 195810 bases at least 0.20 consensus quality: 197810 bases at least 0.20
                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                              130096 153121.
163193 163292: gap of 1442293 201458: contig of 38166
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61355 74139: contig of 12785 bp in length
74140 74239: gap of 100 bp
74240 99150: contig of 24911 bp in length
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1061 1160: gap of 100 bp
1161 2600: contig of 1440 bp in length
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44871: contig of 13922 bp
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15194: contig of 1772 bp in
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24037: contig of 3644 bp in length
37; gap of 100 bp
30849: contig of 6712 bp in length
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10: gap of 100 bp
28820: contig of 20
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61254: contig of 16283 bp in length
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Homo sapiens mRNA; cDNA
Direct Submission
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 759)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTGGCGGCGCACCGGCGATCCACACCGGCGAGAAGCCCTACGTCTGCCCCGACTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCGCAAGAGCCACATCCGGGACGGCGCCTTCTGCTGTGCCATCTGTGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199;
                                                                                                                                                                                                                                                                                                                           SEQUENCE, AC073314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone (DKFZp762K135) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braunschweig/Germany) within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martinsried,
Clone from S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-MAR-2000) MIPS, Am Klopferspitz 18a,
                                   Direct Submission
Submitted (14-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                          2 (bases 1 to 162570)
Waterston, R.H.
                                                                                                                                                                                                                                                                                       HTG;
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd
                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                        Waterston, R.H.
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                     AC073314.2 GI:8954230
 63108,
Jul 7,
                                                                                                                                                                                       (bases
                                                                                                                                                                                                                                                                                   HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from S. Wiemann, Molecular Genome Analysis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKFZp762K135"
/clone_lib="762 (synonym: hmel2). Vector pSport1; host
DH10B; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="melanoma (MeWo cell line)'
246 c 252 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="adult"
                       USA
                                                                                                                                                                                                                                                                                                                                        6 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                         1 to 162570)
2000 this sequence version replaced gi:8516162.
                                                                                                                                                                                                                                                                                                                                                                               162570 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 142.6; DB 7
Pred. No. 4.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 g
                                                                                                                                                                                                                                                                                                                                                            DNA HTG
7 clone RP11-143I21,
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                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 7.94 in Q20 bases; agarose-fp Quality coverage: 8.07 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 164000; agarose-fp Insert size: 162070; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH014312:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome
                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig16
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1: contig of 31734 bp in length
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                                                                                                                              Score 134.6; DB 5
Pred. No. 9.2e-14;
0; Mismatches 164
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least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Sep 19, 1998 this sequence version replaced gi:3213120.
                                                                                                                                                                    University, 4444 Forest Park Avenue, St. Louis, 4 (bases 1 to 128361)
Waterston.P
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                                                                                                                                                                                                                                                                                        Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
AC004877
                                                                                                                                                                                                                Direct Submission Submitted (19-SEP-1998)
                                                                                                                                                                                                                                                Waterston, R.
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Direct Submission
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Unpublished
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Leonard, S., Graves, T.
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                  Contact: sapiens@watson.wustl.edu
Center project name: H_DJ0751H13
                                             Center code: WUGSC Web site: http://gu
                                                                           Center: Washington University Genome Sequencing
                                                                                                                                                 Submission
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                                                                                                                                                                                                                                                                                            Louis,
                                                                                                                                                                                                  USA
                                                                                                                         USA
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NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the MHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc.NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-811N16, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-751H13; actual start of this clone is at base position 1 of RP4-751H13.

CorrectionCorrection**

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H_DJ0751H13.3"
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Center: Washington University Genome Sequencing (center code: WUGSC Web site:http://genome.wustl.edu/gsc/index.shtml
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Query Match
Best Local Similarity
Matches 177; Conserv
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                                                                                                                                                                                                                                                                                                                                                          HTG 15-JUL-2000 HOMO sapiens chromosome 7 clone RP11-428D5, WORKING DRAFT SEQUENCE, 10 unpridered pieces.
                            Direct Submission
Submitted (05-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 15, 2000 this sequence version replaced gi:8990985
                                                                                                                                             Unpublished
                                                                                                                                                                 The sequence of Homo sapiens clone
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210923)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                               AC013273.5 GI:9211421
                                                                                                                                                                                                                                                                                      human.
                                                                                                                            (bases 1 to 210923)
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26933. .29260
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23679. .23794
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67.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (%GC=73.8, o/e=0.90, #CpGs=195)"
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---- Genome Center ----

Sequencing Center

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BASE COUNT
ORIGIN
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Consensus quality: 200595 bases at least Q40
Consensus quality: 204292 bases at least Q30
Consensus quality: 206312 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 4.85 in Q20 bases; agarose-fp Quality coverage: 4.93 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 203000; agarose-fp
Insert size: 210023; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved.
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63763. .104507
                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig9"
4718. .11807
            note="assembly_name:Contig16"
150744 . .210923
/note="assembly_name:Contig17"
51422 c 51731 g 52663 t
                                                                                                                                                    clone_end:SP6
                                                                                 /note="assembly_name:Contig15"
104608. .150643
                                                                                                                                                                  /note="assembly_name:Contig14
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                                                                                                                                                                                                                                                                                                       note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                    note="assembly_name:Contig13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-428D5"
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11807: contig
11907: gap of
20464: contig
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               others
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Query Match Best Local Similarity

28.7%; 67.8%;

Score 126.6; DB 39; Pred. No. 1.6e-12;

Length 210923;

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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-NOV-1990) Denny Chester Beatty Laboratories, 2 (bases 1 to 2094)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2094)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A zinc finger protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denny, P. and Ashworth, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denny,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spermatogenesis; Zfp-29 gene; zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 (2), 221-227 (1991)
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                                  CGKSFSQSSSLIAHQGTHTGEKPYECLTCGESFSWSSNLIKHQRTHTGEKPYRCGDCG
KGFSQRSQLVVHQRTHTGEKPYKCLMCGKSFSRGSILVMHQRAHLGDKPYRCPECGKG
                                                                          SCPECGKSFGNRSSLNTHQGIHTGEKPYACKECGESFSYNSNLIRHQRIHTGEKPYKC
TECGQKFSQSSALITHRRTHTGEKPYQCGECGKNFSRSSNLATHRRTHLVEKPYKCGL
                                                                                                            /translation="MAAEVPAVSTPLSPLVQVPQEEDEQAEVTTMILEDDAWVQEAVL QEDGEESEPPQSAGKGSPQEEDAAEGPQGALVFFRELCRKWLFPEVHTKEQUSHTVLP REIQAWLQEHRPESSEEAVALVEDLTQTFFHSDFEIQSENSNEDMFEQUSHGMF LNISGGEEGQQSDGDSDFERDCGSGGAQGHAPGEDPRVPSBGREVGQLIGLQGTYLG EKPYECPQCGKTFSRKSHLITHERTHTGEKYYKCDECGKSFSDGSNFSHQTTHTGEKPX PXCCDCGKSFSRSANLITHQRIHTGEKPFQCAECGKSFSRSPNLIAHQRTHTGEKPY
                    FSWNSVLIIHQRIHTGEKPYRCPECGKGFSNSSNFITHQRTHLKEKLY"
                                                                                                                                                                                                                                                /protein_id="CAA38920.1"
/db_xref="GI:55471"
                                                                                                                                                                                                                                                                                                                               /gene="Zfp-29"
104. .1948
                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult male"
/tissue_type="testis"
/clone_lib="Lambda ZAP
                                                                                                                                                                                                                                /db_xref="SWISS-PROT:Q07230"
                                                                                                                                                                                                                                                                                         /codon_start=]
                                                                                                                                                                                                                                                                                                         /gene="Zfp-29"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="ssp. domesticus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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237 Fulham Road, LONDON,
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98290545
                                                                                                                                                        Nagase,T., Ishikawa,K., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
Prediction of the coding sequences of unidentified human genes. IX.
The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro
DNA Res. 5 (1), 31-39 (1998)
                                                                                                                                                                                                                                                                       Submitted (13-PBB-1998) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                       Ohara,O., Nagase,T. and Ishikawa,K. Direct Submission
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/note="zinc fingers"
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                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HH1334"
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1. .5627
 /tissue_type="brain"
1. .1483
                              /clone_lib="pBluescriptII
/sex="male"
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                                                  Han, C. and Deaven, L. Sequencing of Human Chromosome
                                                                                    1 (bases 1 to 154218)
Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D.,
Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L.,
Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O.,
Campbell, C., Favcett, J., Maltbie, M., Bussod, M., Sutherland, R.,
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Ricke, D.O.
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                 (bases 1 to 154218)
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cleeepgysteddspettrqlerigoevagprealsrlwelcrwlapelrykedi
lellvlegetyvlpgeigoarverqpesgebayvlveglorkprkhqrgsellsde
vplgiggoflkhqaeaqpedlsleeebarrssqoppaqlshrqqrgpllaper
qQemasaspflsawsqypvlledvavrlsgeeprcmdpaqrbhenecpgiqledgg
Geedaplrmewyrvlsarcqgphplpcqrpapvrglvrpdqprggpppggpspashga
bkfytcpecgkgfsxtshltkhqrthtgerpykclvcgkgfsdrsnssyfsyngtsk
pypcpecgkrfsqssslvihrrthsgrrpyactqckrfennsshfsahrrthtgekpy
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/db_xref="GI:3043638"
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Pred. No. 2.6e-11;
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	íω	/rpt_family="Alu"	/rpt_family="Alu"	/rpt_family="MER42" 1180312101	1158011780	complement(10801.	/rpt_family="Alu	/rpt_family="Alu complement/1040;	996510332)702. 9987 /rnt family="Aln"	/rpt_family="Alu"	/rpt_family="Alu" q515 q812	/rpt_ramity="Ald" 93949682	88089139	79318385	74737776 /rpt_family="Alu	<pre>complement(68486983) /note="GRAIL 2 excellent</pre>	/rpt_family="Alu"		/rpt_family="Alu" 48265155	41984503	complement(3859.		31873504 ′rpt_family="Alu"	/rpt_family="Alu"	/rpt_family="L1"	/rpt_family="Alu"	/rpt_family="Alu" 18712190	/rpt_tam11y="Alu" 15951862	/rpc_ramily="Aid" 14141712	575882	complement(41	/chromosome="16" /clone="RPCI-11 127I20"	/db_xref="taxon:9606"	1154218	M 87545, USA Location/Qualifiers	(08-JAN Litute,	,K., Han,C. and Deaven,L. Submission	Tesmer, J., Mei	Mundt,M., Doggett,N., Munk,C., Saunders,E., Robinson Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L.,	1 to 154218)	Sequenc Analysis	
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LOCUS HSJ599G15 138278 bp DNA HTG 06-OCT-2000 DEFINITION Homo sapiens chromosome 1 clone RP4-599G15 map p12-13.2, ***
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Best Local Similarity
Matches 242; Conserv
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ORGANISM
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Chemistry: Dye-terminator Big Dye; 94% of reads
Chemistry: Dye-primer ramersham; 2% of reads
Chemistry: Dye-primer Big Dye; 1% of reads
Consensus quality: 136114 bases at least 040
Consensus quality: 137176 bases at least 020
Consensus quality: 137544 bases at least 020
Insert size: 137778; sum-of-contigs
Insert size: 136614; 2.3% error; agarose-fp
Quality coverage: 6.30x in 020 bases; sum-of-contigs
Coverage: 8.38x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 25% of reads Sequencing vector: plasmid; L08752; 74% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 14, 2000_this sequence version replaced gi:9588436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138278)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently * consists of 6 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: dJ599G15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: XGAP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                            8020: contig of 8020 bp in length
8021 8120: gap of 100 bp
8121 15996: contig of 7876 bp in length
15997 16096: gap of 100 bp
16097 19055: contig of 2959 bp in length
19056 19155: gap of 100 bp
19156 22087: contig of 2932 bp in length
22188 22187: gap of 100 bp
22188 22998: contig of 7811 bp in length
22998 30098: gap of 100 bp
30099 138278: contig of 108180 bp in length
Location/Qualifiers
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/note="assembly_fragment:02016
fragment_chain:1"
16097. .19055
                                                                 /note="assembly_fragment:01125
fragment_chain:1"
8121. .15996
                                                                                                                                                                                                                                                                                            1. .138278
                                                                                                                                                        /clone="RP4-599G15"
/clone_lib="RPCI-4"
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                        . .8020
                                                                                                                                                                                                   /map="p12-13.
                                                                                                                                                                                                                          'chromosome="]
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AC007518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94153 CCCGTGCCCCGAGTGCGGCGAGGCCTTCAGCCTCAGCTCGCATCTGTTGAGCCACCGGCG
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                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A.,
Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,
Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C.,
Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L.,
Karatas, A., Lehoczky, J., Lieu, C., Locke, K., McLaughlin, J.,
Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B.,
Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,
Tesfaye, S., Torruella-Miller, I., Vassilev, H., Vo, A., Wagner, A.,
Wheeler, I. W. X., Wwan D., Ve W. J. and 70dy M.
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                                            Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus chromosome, clone CT7-345D4
                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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30099 .138278
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22188. .29998
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clone_end:T7
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19156. .22087
  320 Charles Street,
                        (08-MAY-1999) Whitehead
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- clone CT7-345D4,
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head Institute/MIT Center for Genome Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                       gcaagattcacaagog-atccgaggggtcggcccaggccgcccccgggcccggggagcccc 309
                                                                                                                                                                                                                                                                                                                                                                                                                cctacccgtgcaaagagtgcggccgccttccggcacaaaccccaacctgctgtctcaca 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agcgctttaccaataagccctatctgacttcgcaccggcgcatccacacccggcgagaagc 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGCGAGCGGCCGCACGCCTGCCCTGAGTGCGGCAAGAGCTTCATCCGCAAGCACCACT 23188
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                                                                                                                                                                                                                                                                                                                    CATACCCCTGCACGCACTGCCCAAGTGCTTCCGCTACAAACAGTCGCTCAAGTACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197;
                                                                                                           Homo sapiens TTF-I interacting AF000560
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                    Homo sapiens
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                                                                                            AF000560.1
                                                                                                                                                   AF000560
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                                                     numan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 29802: contig of 29802 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
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/db_xref="taxon:10090"
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                                                                                            GI:2145059
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                                                         575
                                                                                                                   515
                                                                                                                                                                      395
                                                                                                                                                                                                                                               | 131 agcgctttaccaataagccctatctgacttcgcaccggcgcatccaccaccggcgcgagaagc 190
                                                                                                                                                                                                                                                                                              335
                                                                                      311
                                                                                                                                  251 gcaagattcacaagcgatccgagggtcggcccaggcccccggccccggcccggggagccccc 310
                                                                                                                                                                                                                                                                                                                                                      275
                                                                                                                                                                                                                                                                                                          71 tgatcgctcaccgcgcgtgcacacggggcgagcggcccaccagtgccccgagtgcggga 130
                                                                                                                                                                                                                                                                                                                                                                    11 ccgtcgaccgccccttccagtgtgcctgttgtggcaagcgcttccggcacaagcccaact 70
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                AGCGCTTCAGCTGGAGCTCCAACCTCATGCAGCACCAGCGCATCCACACGGGCGAGAAGC 454
                  cggcccaggagccgccgccaggggccccgccagagcacccgcagga 416
                                                                                 agctgccagccggccccaggagtccgcggccgagccaccccggcggtacctctgaaac 370
                                                                                                                TGGTGCAGCACCGGCGCATCCACACGGGCGAGAAGCCCTACGCCTGCTTGGAGTGCGGCA 394
                                                                                                                                                                                                                                                                                                                                                   CCGGCGAGCGGCCCAACGCCTGCGCCGACTGCGGCAAGACCTTCTCGCAGAGCTCGCACC 334
CGGCCAAGGTGCTGGCGGCTAGCGTCCGGCGGCCAAGGGGCCCGA
                                                        AGCCCAAGAGCCTCGCGCGTCACCTGCGGCTGCACCCGGAGCTGTCGGGGGCCCTGGCGTGG 634
                                                                                                                                                                                                                                                                                                                                                                                                              226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitted (21-APR-1997) Molecular Biology of the Cell II, German Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg, B.-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jansa, P. and Grummt, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1824)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="TIP20; Transcription Termination Factor
Interacting Peptide 20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="lung"
/cell_type="fibroblasts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell_line="WI-38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-"isolated by yeast two-hybrid screen'
                                                                                                                                                                                                                                                                                                                                                                                                                            26.8%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O
                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 10;
Pred. No. 2.9e-10;
0; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  φ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1824;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
680
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             0;
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